



-90-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liaw, Chen W.  
Lu, Chin-Chun

(ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 63

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Brown, Martin, Haller & McClain  
(B) STREET: 1660 Union Street  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 29-SEPT-97  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/231,193  
(B) FILING DATE: 20-APR-1994  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/052,449  
(B) FILING DATE: 20-APR-1993  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie  
(B) REGISTRATION NUMBER: 33,779  
(C) REFERENCE/DOCKET NUMBER: 6362-9383C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-238-0999  
(B) TELEFAX: 619-238-0062

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3078

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCAGCGAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCA3CC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg 5 Leu Leu Thr Leu Ala 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC A3C GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACC CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	

205					210					215						
ATC Ile 220	ATC Ile 220	CTT Leu 220	TCT Ser 220	GCC Ala 220	AGC Ser 220	GAG Glu 225	GAC Asp 225	GAT Asp 225	GCT Ala 225	GCC Ala 225	ACT Thr 230	GTA Val 230	TAC Tyr 230	CGC Arg 230	GCA Ala 230	963
GCC Ala 235	GCG Ala 235	ATG Met 235	CTG Leu 235	AAC Asn 240	ATG Met 240	ACG Thr 240	GGC Gly 240	TCC Ser 240	GGG Gly 245	TAC Tyr 245	GTG Val 245	TGG Trp 245	CTG Leu 245	GTC Val 250	GGC Gly 250	1011
GAG Glu 255	CGC Arg 255	GAG Glu 255	ATC Ile 255	TCG Ser 255	GGG Gly 255	AAC Asn 255	GCC Ala 260	CTG Leu 260	CGC Arg 260	TAC Tyr 260	GCC Ala 260	CCA Pro 260	GAC Asp 265	GGC Gly 265	ATC Ile 265	1059
CTC Leu 270	GGG Gly 270	CTG Leu 270	CAG Gln 270	CTC Leu 270	ATC Ile 270	AAC Asn 275	GGC Gly 275	AAG Lys 275	AAC Asn 275	GAG Glu 275	TCG Ser 280	GCC Ala 280	CAC His 280	ATC Ile 280	AGC Ser 280	1107
GAC Asp 285	GCC Ala 285	GTG Val 285	GGC Gly 285	GTG Val 285	GTG Val 285	GCC Ala 290	CAG Gln 290	GCC Ala 290	GTG Val 290	CAC His 290	GAG Glu 295	CTC Leu 295	CTC Leu 295	GAG Glu 295	AAG Lys 295	1155
GAG Glu 300	AAC Asn 300	ATC Ile 300	ACC Thr 300	GAC Asp 300	CCG Pro 300	CCG Pro 305	CGG Arg 305	GGC Gly 305	TGC Cys 305	GTG Val 310	GGC Gly 310	AAC Asn 310	ACC Thr 310	AAC Asn 310	ATC Ile 310	1203
TGG Trp 315	AAG Lys 315	ACC Thr 315	GGG Gly 315	CCG Pro 320	CTC Leu 320	TTC Phe 320	AAG Lys 320	AGA Arg 320	GTG Val 325	CTG Leu 325	ATG Met 325	TCT Ser 325	TCC Ser 325	AAG Lys 330	TAT Tyr 330	1251
GCG Ala 335	GAT Asp 335	GGG Gly 335	GTG Val 335	ACT Thr 335	GGT Gly 335	CGC Arg 335	GTG Val 340	GAG Glu 340	TTC Phe 340	AAT Asn 340	GAG Glu 340	GAT Asp 345	GGG Gly 345	GAC Asp 345	CGG Arg 345	1299
AAG Lys 350	TTC Phe 350	GCC Ala 350	AAC Asn 350	TAC Tyr 350	AGC Ser 350	ATC Ile 355	ATG Met 355	AAC Asn 355	CTG Leu 355	CAG Gln 355	AAC Asn 360	CGC Arg 360	AAG Lys 360	CTG Leu 360	GTG Val 360	1347
CAA Gln 365	GTG Val 365	GGC Gly 365	ATC Ile 365	TAC Tyr 365	AAT Asn 365	GGC Gly 370	ACC Thr 370	CAC His 370	GTG Val 370	ATC Ile 370	CCT Pro 375	AAT Asn 375	GAC Asp 375	AGG Arg 375	AAG Lys 375	1395
ATC Ile 380	ATC Ile 380	TGG Trp 380	CCA Pro 380	GGC Gly 380	GGA Gly 380	GAG Glu 385	ACA Thr 385	GAG Glu 385	AAG Lys 385	CCT Pro 390	CGA Arg 390	GGG Gly 390	TAC Tyr 390	CAG Gln 390	ATG Met 390	1443
TCC Ser 395	ACC Thr 395	AGA Arg 395	CTG Leu 395	AAG Lys 400	ATT Ile 400	GTG Val 400	ACG Thr 400	ATC Ile 400	CAC His 405	CAG Gln 405	GAG Glu 405	CCC Pro 405	TTC Phe 405	GTG Val 410	TAC Tyr 410	1491
GTG Val 415	AAG Lys 415	CCC Pro 415	ACG Thr 415	CTG Leu 415	AGT Ser 415	GAT Asp 415	GGG Gly 420	ACA Thr 420	TGC Cys 420	AAG Lys 420	GAG Glu 420	GAG Glu 420	TTC Phe 425	ACA Thr 425	GTG Val 425	1539
AAC Asn 430	GGC Gly 430	GAC Asp 430	CCA Pro 430	GTC Val 430	AAG Lys 430	AAG Lys 435	GTG Val 435	ATC Ile 435	TGC Cys 435	ACC Thr 435	GGG Gly 435	CCC Pro 440	AAC Asn 440	GAC Asp 440	ACG Thr 440	1587
TCC Ser 445	CCG Pro 445	GGC Gly 445	AGC Ser 445	CCC Pro 445	CGC Arg 445	CAC His 450	ACG Thr 450	GTG Val 450	CCT Pro 450	CAG Gln 450	TGT Cys 455	TGC Cys 455	TAC Tyr 455	GGC Gly 455	TTT Phe 455	1635
TGC Cys 460	ATC Ile 460	GAC Asp 460	CTG Leu 460	CTC Leu 460	ATC Ile 465	AAG Lys 465	CTG Leu 465	GCA Ala 465	CGG Arg 465	ACC Thr 465	ATG Met 470	AAC Asn 470	TTC Phe 470	ACC Thr 470	TAC Tyr 470	1683

GAG	GTG	CAG	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
475					480					485					490	
AAC	AAC	ACC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
				495					500					505		
AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
			510					515					520			
CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
		525					530					535				
ACT	ATT	CTG	GTG	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
	540					545					550					
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
555					560					565					570	
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCG	TTC	2019
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
				575					580					585		
GGC	CCG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	
			590					595					600			
CTG	TCC	TCC	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
		605					610					615				
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
	620					625					630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
635					640					645					650	
CTG	GCC	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655					660					665		
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
			670					675					680			
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
		685					690					695				
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
	700					705					710					
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	
715					720					725					730	
TGG	GAC	TCC	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	
				735					740					745		





GCTAACTGCC	CCCAGGCGGA	GGGGCTTGG	GCAGAGACGG	CAGCCCCATC	CTTCCCCGAG	3735
CACCAGCCTG	AGCCACAGTG	GGCCCCATGG	CCCCAGCTGG	CTGGGTGGCC	CCTCCTCGGG	3795
CGCCTGCGGT	CCTCTGCAGC	CTGAGCTCCA	CCCTCCCCCTC	TTCTTGGGGC	ACCGCCCCACC	3855
AAACACCCCG	TCTGCCCCCTT	GACGCCACAC	GCCGGGGCTG	GCGCTGCCCT	CCCCCACGGC	3915
CGTCCCTGAC	TTCCCAGCTG	GCAGCGCCTC	CCGCGGCCTC	GGGCGGCCTC	CTCCAGAATC	3975
GAGAGGGCTG	AGCCCCCTCT	CTCCTCGTCC	GGCCTGCAGC	ACAGAAGGGG	GCCTCCCCGG	4035
GGGTCCCCGG	ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	GGGCACGGGA	4095
GAGCGCCACC	CGCCCCCCCC	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCCC	CCACCTTGTA	4155
CAGAACCCAGC	ACTCCCAGGG	CCCGAGCGCG	TGCCTTCCCC	GTGCGCAGCC	GCGCTCTGCC	4215
CCTCCGTCCC	CAGGGTGCAG	GCGCGCACCG	CCCAACCCCC	ACCTCCCGGT	GTATGCAGTG	4275
GTGATGCCTA	AAGGAATGTC	ACG				4298

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 938 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
	20							25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
	35						40					45			
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50					55					60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65				70			75						80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
			85					90						95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
		100					105						110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
	115					120					125				
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
	130					135				140					
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
	145				150				155						160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
			165					170						175	

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly  
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met  
500 505 510

Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu  
515 520 525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys

530		535		540
Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser 545 550 555 560				
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met 565 570 575				
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn 580 585 590				
Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp 595 600 605				
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro 610 615 620				
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala 625 630 635 640				
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val 645 650 655				
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu 660 665 670				
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser 675 680 685				
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg 690 695 700				
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala 705 710 715 720				
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu 725 730 735				
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu 740 745 750				
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp 755 760 765				
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe 770 775 780				
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser 785 790 795 800				
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val 805 810 815				
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe 820 825 830				
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met 835 840 845				
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp 850 855 860				
Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe 865 870 875 880				
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser				

395

Leu Gln Leu Cys Ser Arg His Arg Glu Ser  
930 935

(11) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME KEY: CDS

(B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCTAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CSGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CCG GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CCG CTG CTG GAC GTG GTC ACC CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	
GGG CCG CGC GCG CCG ACC CAG CCG CTG CTG CCG CAG CTC GAC GCG CCC	854
Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	

210								215				220				
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
		240				245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
		255			260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
		320				325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GST	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
		335			340					345					350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTC	GGG	CGC	TGG	GAG	CAT	GSC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370				375						380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAT	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
		400				405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GCC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
		415			420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	ASC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTG	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				
ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GCC	GTA	TGG	AAC	GGC	ATG	1670

Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
480						485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Gln	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
495					500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACC	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCC	GGC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
			545				550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
575					580					585					590	
AAG	TCC	GGG	GGC	CCA	GCT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	2006
Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	
				595					600					605		
TGG	GGG	CTG	GTG	TTC	AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	2054
Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	
			610					615					620			
ACC	ACC	AGC	AAG	ATC	ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	2102
Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	
			625				630					635				
TTC	CTC	GCC	AGA	TAC	ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	2150
Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	
	640					645					650					
CAA	TAC	ATC	GAC	ACT	GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	2198
Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	
655					660				665						670	
CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	2246
Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	
				675					680					685		
AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAT	2294
Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	
			690					695					700			
ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	GAG	GAC	GGG	CTC	ACC	AGC	CTC	2342
Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	
		705					710					715				
AAG	ATG	GGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	2390
Lys	Met	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	
		720				725					730					
TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	2438
Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	
735					740					745					750	



GGC	AAG	GTC	TTT	GCT	ACC	ACT	GAC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	2486
Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	
				755					760					765		
TCC	CAC	TGG	AAG	CGG	GGC	ATA	GAT	CTG	GGC	CTC	TTG	CAG	TTC	CTG	GGG	2534
Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	
			770					775					780			
GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	2582
Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	
		785					790					795				
CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	2630
Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	
	800					805					810					
ATG	GGA	GGC	GTC	TTC	TAC	ATG	CTG	CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	2678
Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	
	815				820					825					830	
CTG	GTC	TTC	GCC	TGG	GAG	CAC	CTG	GTC	TAC	TGG	AAG	CTG	CGC	CAC	TGC	2726
Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	
				835					840					845		
GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	2774
Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	
			850					855					860			
ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	2822
Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	
		865				870						875				
CAG	GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TGC	GCC	CAG	GCC	AGC	GTG	CTC	2870
Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	
	880					885					890					
AAG	ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	2918
Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	
	895				900				905						910	
AAC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	2966
Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	
				915					920					925		
CGC	CCT	GCG	CCC	CCA	CCG	TCC	CCG	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	3014
Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	
			930					935					940			
AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	TCC	CCC	CCA	GAG	CCG	AGC	CCC	ACC	3062
Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	
		945					950					955				
GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	3110
Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	
	960					965					970					
CCG	CAG	CCC	CCG	GGG	CGC	CCC	CCG	ACC	CCG	GGG	CCG	CCC	CTG	TCC	GAC	3158
Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	
	975				980					985					990	
GTC	TCC	CGA	GTG	TCC	CGC	CGC	CCA	CCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	3206
Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	
			995					1000						1005		
CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TGC	GCC	TCC	GAG	CGG	CCC	CTG	3254
Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	
			1010					1015					1020			

TGG CGC GCG CGC TGT CAG TAC AGC TCC TTT CCT CGA GGC GAG CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GGC CGC GGC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CCG CCG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
AAC GCG GCC TGG GCC CCG GGC TCG CGC CCG AGT CAC GGT TCC CTG CCC Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GGT CCG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCC GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CCG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GGC GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC ACT GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala 1200 1205 1210	3830
CGT GGG ACC CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CCG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCGGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAAGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG	3986
GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA	4046
TCAATGACCT CAGCTAGCCT CA	4068

2. INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1236 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Gly	Ala	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Leu	Phe	Gly
1				5					10					15	
Ala	Trp	Ala	Gly	Leu	Gly	Pro	Gly	Gln	Gly	Glu	Gln	Gly	Met	Thr	Val
			20					25					30		
Ala	Val	Val	Phe	Ser	Ser	Ser	Gly	Pro	Pro	Gln	Ala	Gln	Phe	Arg	Val
		35					40					45			
Arg	Leu	Thr	Pro	Gln	Ser	Phe	Leu	Asp	Leu	Pro	Leu	Glu	Ile	Gln	Pro
	50					55					60				
Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	Ser	Leu	Leu	Thr	Gln
65					70					75					80
Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	Gly	Ile	Val	Phe	Glu
			85					90						95	
Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser
		100						105					110		
Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	Ala	Val
		115					120					125			
Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	Gly	Val
	130					135					140				
Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	Glu	Tyr
145					150					155					160
Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	His	Ala
			165						170					175	
Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	Val	Ser
		180						185					190		
Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	Gly	Pro
		195					200					205			
Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	Val	Phe
	210					215					220				
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala
225					230					235					240
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn
			245						250					255	
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly
		260					265						270		
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys
		275					280						285		
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp
	290				295						300				
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His
305					310					315					320

Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu
				325					330					335	
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr
			340					345					350		
Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu
		355					360					365			
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr
	370					375					380				
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser
385					390					395					400
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val
				405					410					415	
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro
			420					425					430		
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro
			435				440					445			
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys
	450					455					460				
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn
465					470					475					480
Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly
				485					490					495	
Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile
			500					505					510		
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu
		515					520					525			
Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro
	530					535					540				
Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe
545					550				555						560
Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr
				565					570					575	
Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser
			580					585					590		
Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala
		595					600					605			
Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr
	610					615					620				
Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu
625					630				635						640
Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr
				645					650					655	
Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln
			660					665					670		

Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	675	680	685
Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	690	695	700
Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	705	710	715
Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	725	730	735
Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	740	745	750
Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	755	760	765
Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	770	775	780
Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	785	790	795
Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	805	810	815
Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	820	825	830
Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	835	840	845
Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	850	855	860
Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	865	870	875
Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	885	890	895
Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	900	905	910
Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	915	920	925
Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	930	935	940
Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	945	950	955
Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	965	970	975
Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	980	985	990
Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	995	1000	1005
Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	1010	1015	1020

-107-

Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg  
1025 1030 1035 1040

Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro  
1045 1050 1055

Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala  
1060 1065 1070

Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser  
1075 1080 1085

Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr  
1090 1095 1100

Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu  
1105 1110 1115 1120

Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln  
1125 1130 1135

Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val  
1140 1145 1150

Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys  
1155 1160 1165

Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala  
1170 1175 1180

Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly  
1185 1190 1195 1200

Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly  
1205 1210 1215

Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu  
1220 1225 1230

Glu Ser Glu Val  
1235

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(11) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME, KEY: CDS
- (B) LOCATION: 2..22

(x) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG  
Ser Glu Ala Gln Pro Val Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4808 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT A3CC3CCCCC CGTGGGGGGG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGG3C CGA3CATGC GGGAACCCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG C3CA3CGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGBACCGTC	300
AGTGGCGACT ATG 33C AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG	349
Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro	
1 5 10	
GCC CTT CTG GTC TGG CGC 33T CCG GCG CCG AGC GCG GCG GCG GAG AAG	397
Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys	
15 20 25	
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC	445

Gly 30	Pro	Pro	Ala	Leu	Asn 35	Ile	Ala	Val	Met	Leu 40	Gly	His	Ser	His	Asp 45	
GTG	ACA	GAG	CGC	GAA	CTT	CGA	ACA	CTG	TGG	GGC	CCC	GAG	CAG	GCG	GCG	493
Val	Thr	Glu	Arg	Glu 50	Leu	Arg	Thr	Leu	Trp 55	Gly	Pro	Glu	Gln	Ala	Ala	
GGG	CTG	CCC	CTG	GAC	GTG	AAC	GTG	GTA	GCT	CTG	CTG	ATG	AAC	CGC	ACC	541
Gly	Leu	Pro	Leu 65	Asp	Val	Asn	Val	Val 70	Ala	Leu	Leu	Met	Asn 75	Arg	Thr	
GAC	CCC	AAG	AGC	CTC	ATC	ACG	CAC	GTG	TGC	GAC	CTC	ATG	TCC	GGG	GCA	589
Asp	Pro	Lys 80	Ser	Leu	Ile	Thr	His 85	Val	Cys	Asp	Leu	Met	Ser 90	Gly	Ala	
CGC	ATC	CAC	GGC	CTC	GTG	TTT	GCG	GAC	GAC	ACG	GAC	CAG	GAG	GCC	GTA	637
Arg	Ile 95	His	Gly	Leu	Val	Phe 100	Gly	Asp	Asp	Thr	Asp 105	Gln	Glu	Ala	Val	
GCC	CAG	ATG	CTG	GAT	TTT	ATC	TCC	TCC	CAC	ACC	TTC	GTC	CCC	ATC	TTG	685
Ala	Gln	Met	Leu	Asp	Phe 115	Ile	Ser	Ser	His	Thr 120	Phe	Val	Pro	Ile	Leu 125	
GGC	ATT	CAT	GCG	GGC	GCA	TCT	ATG	ATC	ATG	GCT	GAC	AAG	GAT	CCG	ACG	733
Gly	Ile	His	Gly 130	Gly	Ala	Ser	Met	Ile 135	Met	Ala	Asp	Lys	Asp	Pro	Thr 140	
TCT	ACC	TTC	TTC	CAG	TTT	GGA	GCG	TCC	ATC	CAG	CAG	CAA	GCC	ACG	GTC	781
Ser	Thr	Phe 145	Gln	Phe	Gly	Ala	Ser 150	Ile	Gln	Gln	Gln	Ala 155	Thr	Val		
ATG	CTG	AAG	ATC	ATG	CAG	GAT	TAT	GAC	TGG	CAT	GTC	TTC	TCC	CTG	GTG	829
Met	Leu	Lys 160	Ile	Met	Gln	Asp	Tyr 165	Asp	Trp	His	Val 170	Phe	Ser	Leu	Val	
ACC	ACT	ATC	TTC	CCT	GGC	TAC	AGG	GAA	TTC	ATC	AGC	TTC	GTC	AAG	ACC	877
Thr	Thr	Ile 175	Phe	Pro	Gly	Tyr 180	Arg	Glu	Phe	Ile 185	Ser	Phe	Val	Lys	Thr	
ACA	GTG	GAC	AAC	AGC	TTT	GTG	GGC	TGG	GAC	ATG	CAG	AAT	GTG	ATC	ACA	925
Thr	Val	Asp	Asn	Ser	Phe 195	Val	Gly	Trp	Asp 200	Met	Gln	Asn	Val	Ile	Thr 205	
CTG	GAC	ACT	TCC	TTT	GAG	GAT	GCA	AAG	ACA	CAA	GTC	CAG	CTG	AAG	AAG	973
Leu	Asp	Thr	Ser 210	Phe	Glu	Asp	Ala	Lys 215	Thr	Gln	Val	Gln	Leu	Lys 220	Lys	
ATC	CAC	TCT	TCT	GTC	ATC	TTG	CTC	TAC	TGT	TCC	AAA	GAC	GAG	GCT	GTT	1021
Ile	His	Ser	Ser 225	Val	Ile	Leu	Leu 230	Tyr	Cys	Ser	Lys	Asp 235	Glu	Ala	Val	
CTC	ATT	CTG	AGT	GAG	GCC	CGC	TCC	CTT	GGC	CTC	ACC	GGG	TAT	GAT	TTC	1069
Leu	Ile	Leu	Ser 240	Glu	Ala	Arg	Ser 245	Leu	Gly	Leu	Thr	Gly 250	Tyr	Asp	Phe	
TTC	TGG	ATT	GTC	CCC	AGC	TTG	GTC	TCT	GGG	AAC	ACG	GAG	CTC	ATC	CCA	1117
Phe	Trp	Ile 255	Val	Pro	Ser	Leu 260	Val	Ser	Gly	Asn 265	Thr	Glu	Leu	Ile	Pro	
AAA	GAG	TTT	CCA	TGG	GGA	CTC	ATT	TCT	GTC	TCC	TAC	GAT	GAC	TGG	GAC	1165
Lys	Glu	Phe 270	Pro	Ser	Gly 275	Leu	Ile	Ser	Val 280	Ser	Tyr	Asp	Asp	Trp	Asp 285	
TAC	AGC	CTG	GAG	GCG	AGA	GTG	AGG	GAC	GGC	ATT	GGC	ATC	CTA	ACC	ACC	1213
Tyr	Ser	Leu	Glu 290	Ala	Arg	Val	Arg	Asp	Gly 295	Ile	Gly	Ile	Leu	Thr 300	Thr	



GCT	GCA	TCT	TCT	ATG	ATG	GAG	AAG	TTC	TCC	TAC	ATC	CCC	GAG	GCC	AAG	1261
Ala	Ala	Ser	Ser	Met	Leu	Glu	Lys	Phe	Ser	Tyr	Ile	Pro	Glu	Ala	Lys	
		305						310					315			
GCC	AGC	TGC	TAC	GGG	GAG	ATG	GAG	AGG	CCA	GAG	GTC	CCG	ATG	CAC	ACC	1309
Ala	Ser	Cys	Tyr	Gly	Gln	Met	Glu	Arg	Pro	Glu	Val	Pro	Met	His	Thr	
		320					325					330				
TTG	CAC	CCA	TTT	ATG	GTC	AAT	GTT	ACA	TGG	GAT	GGC	AAA	GAC	TTA	TCC	1357
Leu	His	Pro	Phe	Met	Val	Asn	Val	Thr	Trp	Asp	Gly	Lys	Asp	Leu	Ser	
	335					340					345					
TTC	ACT	GAG	GAA	GGC	TAC	CAG	GTG	CAC	CCC	AGG	CTG	GTG	GTG	ATT	GTG	1405
Phe	Thr	Glu	Glu	Gly	Tyr	Gln	Val	His	Pro	Arg	Leu	Val	Val	Ile	Val	
	350				355					360					365	
CTG	AAC	AAA	GAC	CGG	GAA	TGG	GAA	AAG	GTG	GGC	AAG	TGG	GAG	AAC	CAT	1453
Leu	Asn	Lys	Asp	Arg	Glu	Trp	Glu	Lys	Val	Gly	Lys	Trp	Glu	Asn	His	
				370					375					380		
ACG	CTG	AGC	CTG	AGG	CAC	GCC	GTG	TGG	CCC	AGG	TAC	AAG	TCC	TTC	TCC	1501
Thr	Leu	Ser	Leu	Arg	His	Ala	Val	Trp	Pro	Arg	Tyr	Lys	Ser	Phe	Ser	
			385					390					395			
GAC	TGT	GAG	CCG	GAT	GAC	AAC	CAT	CTC	AGC	ATC	GTC	ACC	CTG	GAG	GAG	1549
Asp	Cys	Glu	Pro	Asp	Asp	Asn	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	
		400					405					410				
GCC	CCA	TTC	GTC	ATC	GTG	GAA	GAC	ATA	GAC	CCC	CTG	ACC	GAG	ACG	TGT	1597
Ala	Pro	Phe	Val	Ile	Val	Glu	Asp	Ile	Asp	Pro	Leu	Thr	Glu	Thr	Cys	
		415				420					425					
GTG	AGG	AAC	ACC	GTG	CCA	TGT	CGG	AAG	TTC	GTC	AAA	ATC	AAC	AAT	TCA	1645
Val	Arg	Asn	Thr	Val	Pro	Cys	Arg	Lys	Phe	Val	Lys	Ile	Asn	Asn	Ser	
	430				435					440					445	
ACC	AAT	GAG	GGG	ATG	AAT	GTG	AAG	AAA	TGC	TGC	AAG	GGG	TTC	TGC	ATT	1693
Thr	Asn	Glu	Gly	Met	Asn	Val	Lys	Lys	Cys	Cys	Lys	Gly	Phe	Cys	Ile	
				450					455					460		
GAT	ATT	CTG	AAG	AAG	CTT	TCC	AGA	ACT	GTG	AAG	TTT	ACT	TAC	GAC	CTC	1741
Asp	Ile	Leu	Lys	Lys	Leu	Ser	Arg	Thr	Val	Lys	Phe	Thr	Tyr	Asp	Leu	
			465					470					475			
TAT	CTG	GTG	ACC	AAT	GGG	AAG	CAT	GGC	AAG	AAA	GTT	AAC	AAT	GTG	TGG	1789
Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Lys	Val	Asn	Asn	Val	Trp	
		480					485					490				
AAT	GGA	ATG	ATC	GGT	GAA	GTG	GTC	TAT	CAA	CGG	GCA	GTC	ATG	GCA	GTT	1837
Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Tyr	Gln	Arg	Ala	Val	Met	Ala	Val	
		495				500					505					
GGC	TGG	CTC	ACC	ATC	AAT	GAG	GAA	CGT	TCT	GAA	GTG	GTG	GAC	TTC	TCT	1885
Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Val	Val	Asp	Phe	Ser	
		510			515					520					525	
GTG	CCC	TTT	GTG	GAA	ACG	GGA	ATC	AGT	GTC	ATG	GTT	TCA	AGA	AGT	AAT	1933
Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ser	Arg	Ser	Asn	
				530				535						540		
GGC	ACC	GTC	TCA	CCT	TCT	GCT	TTT	CTA	GAA	CCA	TTC	AGC	GCC	TCT	GTC	1981
Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Ser	Val	
			545					550					555			
TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATT	GTT	TCT	GCC	ATA	GCT	GTT	2029
Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Ile	Ala	Val	
		560					565					570				

TGG	STC	TTG	GAT	TAC	TCC	AGC	CCT	STT	GGA	TAC	AAC	AGA	AAC	TTA	GCC	2077
Trp	Val	Leu	Asp	Tyr	Ser	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	
575						580					585					
AAA	GGG	AAA	GCA	CCC	CAT	GGG	CCT	TCT	TTT	ACA	ATT	GGA	AAA	GCT	ATA	2125
Lys	Gly	Lys	Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	
590					595					600					605	
TGG	CTT	CTT	TGG	GGC	CTG	GTG	TTC	AAT	AAC	TCC	GTG	CCT	GTC	CAG	AAT	2173
Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	
				610					615					620		
CCT	AAA	GGG	ACC	ACC	AGC	AAG	ATC	ATG	GTA	TCT	GTA	TGG	GCC	TTC	TTC	2221
Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	
			625					630					635			
GCT	GTC	ATA	TTC	CTG	GCT	AGC	TAC	ACA	GCC	AAT	CTG	GCT	GCC	TTC	ATG	2269
Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	
		640					645					650				
ATC	CAA	GAG	GAA	TTT	GTG	GAC	CAA	GTG	ACC	GGC	CTC	AGT	GAC	AAA	AAG	2317
Ile	Gln	Glu	Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	
	655					660					665					
TTT	CAG	AGA	CCT	CAT	GAC	TAT	TCC	CCA	CCT	TTT	CGA	TTT	GGG	ACA	GTG	2365
Phe	Gln	Arg	Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	
670					675					680					685	
CCT	AAT	GGA	AGC	ACG	GAG	AGA	AAC	ATT	CGG	AAT	AAC	TAT	CCC	TAC	ATG	2413
Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	
				690					695					700		
CAT	CAG	TAC	ATG	ACC	AAA	TTT	AAT	CAG	AAA	GGA	GTA	GAG	GAC	GCC	TTG	2461
His	Gln	Tyr	Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	
			705					710					715			
GTC	AGC	CTG	AAA	ACG	GGG	AAG	CTG	SAC	GCT	TTC	ATC	TAC	GAT	GCC	GCA	2509
Val	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
		720					725					730				
GTC	TTG	AAT	TAC	AAG	GCT	GGG	AGG	SAT	GAA	GGC	TGC	AAG	CTG	GTG	ACC	2557
Val	Leu	Asn	Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
	735					740					745					
ATC	GGG	AGT	GGG	TAC	ATC	TTT	GCC	ACC	ACC	GCT	TAT	GGA	ATT	GCC	CTT	2605
Ile	Gly	Ser	Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	
750					755					760					765	
CAG	AAA	GGC	TCT	CCT	TGG	AAG	AGG	CAG	ATC	SAC	CTG	GCC	TTG	CTT	CAG	2653
Gln	Lys	Gly	Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
				770					775						780	
TTT	GTG	GGT	GAT	GGT	GAG	ATG	GAG	GAG	CTG	GAG	ACC	CTG	TGG	CTC	ACT	2701
Phe	Val	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	
			785					790					795			
GGG	ATC	TGC	CAC	AAC	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	CAG	CTG	GAC	2749
Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	
		800					805					810				
ATT	GAC	AAC	ATG	GCG	GGC	GTA	TTC	TAC	ATG	CTG	GCT	GCC	GCC	ATG	GCC	2797
Ile	Asp	Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Ala	Ala	Ala	Met	Ala	
	815					820					825					
CTT	AGC	CTC	ATC	ACC	TTC	ATC	TGG	GAG	CAC	CTC	TTC	TAC	TGG	AAG	CTG	2845
Leu	Ser	Leu	Ile	Thr	Phe	Ile	Trp	Glu	His	Leu	Phe	Tyr	Trp	Lys	Leu	
830					835					840					845	

CGC	TTC	TGT	TTC	ACG	GGC	GTG	TGC	TCC	GAC	CGG	CCT	GGG	TTG	CTC	TTC	2893
Arg	Phe	Cys	Phe	Thr	Gly	Val	Cys	Ser	Asp	Arg	Pro	Gly	Leu	Leu	Phe	
				850					855					860		
TCC	ATC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	ATT	CAT	GGA	GTG	CAC	ATT	GAA	2941
Ser	Ile	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	His	Ile	Glu	
			865					870					875			
GAA	AAG	AAG	AAG	TCT	CCA	GAC	TTC	AAT	CTG	ACG	GGA	TCC	CAG	AGC	AAC	2989
Glu	Lys	Lys	Lys	Ser	Pro	Asp	Phe	Asn	Leu	Thr	Gly	Ser	Gln	Ser	Asn	
			880				885					890				
ATG	TTA	AAA	CTC	CTC	CGG	TCA	GCC	AAA	AAC	ATT	TCC	AGC	ATG	TCC	AAC	3037
Met	Leu	Lys	Leu	Leu	Arg	Ser	Ala	Lys	Asn	Ile	Ser	Ser	Met	Ser	Asn	
	895					900					905					
ATG	AAC	TCC	TCA	AGA	ATG	GAC	TCA	CCC	AAA	AGA	GCT	GCT	GAC	TTC	ATC	3085
Met	Asn	Ser	Ser	Arg	Met	Asp	Ser	Pro	Lys	Arg	Ala	Ala	Asp	Phe	Ile	
	910				915					920					925	
CAA	AGA	GGT	TCC	CTC	ATC	ATG	GAC	ATG	GTT	TCA	GAT	AAG	GGG	AAT	TTG	3133
Gln	Arg	Gly	Ser	Leu	Ile	Met	Asp	Met	Val	Ser	Asp	Lys	Gly	Asn	Leu	
				930					935					940		
ATG	TAC	TCA	GAC	AAC	AGG	TCC	TTT	CAG	GGG	AAA	GAG	AGC	ATT	TTT	GGA	3181
Met	Tyr	Ser	Asp	Asn	Arg	Ser	Phe	Gln	Gly	Lys	Glu	Ser	Ile	Phe	Gly	
			945					950					955			
GAC	AAC	ATG	AAC	GAA	CTC	CAA	ACA	TTT	GTG	GCC	AAC	CGG	CAG	AAG	GAT	3229
Asp	Asn	Met	Asn	Glu	Leu	Gln	Thr	Phe	Val	Ala	Asn	Arg	Gln	Lys	Asp	
		960					965					970				
AAC	CTC	AAT	AAC	TAT	GTA	TTC	CAG	GGA	CAA	CAT	CCT	CTT	ACT	CTC	AAT	3277
Asn	Leu	Asn	Asn	Tyr	Val	Phe	Gln	Gly	Gln	His	Pro	Leu	Thr	Leu	Asn	
	975					980					985					
GAG	TCC	AAC	CCT	AAC	ACG	GTG	GAG	GTG	GCC	GTG	AGC	ACA	GAA	TCC	AAA	3325
Glu	Ser	Asn	Pro	Asn	Thr	Val	Glu	Val	Ala	Val	Ser	Thr	Glu	Ser	Lys	
	990				995				1000						1005	
GCG	AAC	TCT	AGA	CCC	CGG	CAG	CTG	TGG	AAG	AAA	TCC	GTG	GAT	TCC	ATA	3373
Ala	Asn	Ser	Arg	Pro	Arg	Gln	Leu	Trp	Lys	Lys	Ser	Val	Asp	Ser	Ile	
			1010						1015					1020		
CGC	CAG	GAT	TCA	CTA	TCC	CAG	AAT	CCA	GTC	TCC	CAG	AGG	GAT	GAG	GCA	3421
Arg	Gln	Asp	Ser	Leu	Ser	Gln	Asn	Pro	Val	Ser	Gln	Arg	Asp	Glu	Ala	
			1025					1030					1035			
ACA	GCA	GAG	AAT	AGG	ACC	CAC	TCC	CTA	AAG	AGC	CCT	AGG	TAT	CTT	CCA	3469
Thr	Ala	Glu	Asn	Arg	Thr	His	Ser	Leu	Lys	Ser	Pro	Arg	Tyr	Leu	Pro	
		1040					1045					1050				
GAA	GAG	ATG	GCC	CAC	TCT	GAC	ATT	TCA	GAA	ACG	TCA	AAT	CGG	GCC	ACG	3517
Glu	Glu	Met	Ala	His	Ser	Asp	Ile	Ser	Glu	Thr	Ser	Asn	Arg	Ala	Thr	
	1055					1060					1065					
TGC	CAC	AGG	GAA	CCT	GAC	AAC	AGT	AAG	AAC	CAC	AAA	ACC	AAG	GAC	AAC	3565
Cys	His	Arg	Glu	Pro	Asp	Asn	Ser	Lys	Asn	His	Lys	Thr	Lys	Asp	Asn	
	1070				1075				1080						1085	
TTT	AAA	AGG	TCA	GTG	GCC	TCC	AAA	TAC	CCC	AAG	GAC	TGT	AGT	GAG	GTG	3613
Phe	Lys	Arg	Ser	Val	Ala	Ser	Lys	Tyr	Pro	Lys	Asp	Cys	Ser	Glu	Val	
			1090						1095					1100		
GAG	CGC	ACC	TAC	CTG	AAA	ACC	AAA	TCA	AGC	TCC	CCT	AGA	GAC	AAG	ATC	3661
Glu	Arg	Thr	Tyr	Leu	Lys	Thr	Lys	Ser	Ser	Ser	Pro	Arg	Asp	Lys	Ile	
			1105					1110					1115			

-113-

TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAG CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381
TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477

TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG	4525
Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu	
1390 1395 1400 1405	
AGG TCA ACC GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT	4573
Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp	
1410 1415 1420	
GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT	4621
Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn	
1425 1430 1435	
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG	4669
Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val	
1440 1445 1450	
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT	4722
Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val	
1455 1460 146	
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC	4782
AATAGTGCCC TGCTAAGAGG AAGGAG	4803

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu	
1 5 10 15	
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro	
20 25 30	
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu	
35 40 45	
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro	
50 55 60	
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys	
65 70 75 80	
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His	
85 90 95	
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met	
100 105 110	
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His	
115 120 125	
Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe	
130 135 140	
Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys	
145 150 155 160	
Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile	

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Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ser	Arg	Ser	Asn	Gly	Thr	Val	530	535	540
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Ser	Val	Trp	Val	Met	545	550	555
Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Ile	Ala	Val	Trp	Val	Leu	565	570	575
Asp	Tyr	Ser	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	Lys	Gly	Lys	580	585	590
Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	Trp	Leu	Leu	595	600	605
Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	Pro	Lys	Gly	610	615	620
Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	625	630	635
Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	645	650	655
Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	660	665	670
Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	675	680	685
Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	His	Gln	Tyr	690	695	700
Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	Val	Ser	Leu	705	710	715
Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	725	730	735
Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	740	745	750
Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	Gln	Lys	Gly	755	760	765
Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Val	Gly	770	775	780
Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	Gly	Ile	Cys	785	790	795
His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	Ile	Asp	Asn	805	810	815
Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Ala	Ala	Ala	Met	Ala	Leu	Ser	Leu	820	825	830
Ile	Thr	Phe	Ile	Trp	Glu	His	Leu	Phe	Tyr	Trp	Lys	Leu	Arg	Phe	Cys	835	840	845
Phe	Thr	Gly	Val	Cys	Ser	Asp	Arg	Pro	Gly	Leu	Leu	Phe	Ser	Ile	Ser	850	855	860
Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	His	Ile	Glu	Glu	Lys	Lys	865	870	875
Lys	Ser	Pro	Asp	Phe	Asn	Leu	Thr	Gly	Ser	Gln	Ser	Asn	Met	Leu	Lys			

885	890	895
Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser 900 905 910		
Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly 915 920 925		
Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser 930 935 940		
Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met 945 950 955 960		
Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn 965 970 975		
Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn 980 985 990		
Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser 995 1000 1005		
Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp 1010 1015 1020		
Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu 1025 1030 1035 1040		
Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met 1045 1050 1055		
Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg 1060 1065 1070		
Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg 1075 1080 1085		
Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr 1090 1095 1100		
Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile 1105 1110 1115 1120		
Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val 1125 1130 1135		
Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln 1140 1145 1150		
Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn 1155 1160 1165		
Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr 1170 1175 1180		
Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His 1185 1190 1195 1200		
Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser 1205 1210 1215		
Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser 1220 1225 1230		
Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile 1235 1240 1245		



-118-

Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu  
 1250 1255 1260

Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln  
 1265 1270 1275 1280

Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val  
 1285 1290 1295

Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser  
 1300 1305 1310

Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu  
 1315 1320 1325

Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe  
 1330 1335 1340

Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp  
 1345 1350 1355 1360

His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg  
 1365 1370 1375

Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro  
 1380 1385 1390

Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr  
 1395 1400 1405

Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile  
 1410 1415 1420

Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser  
 1425 1430 1435 1440

Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu  
 1445 1450 1455

Met Pro Ser Ile Glu Ser Asp Val  
 1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCTTCC CCTCGGACC  
 CTCGGGTGGA CATG

60

74

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3155 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGGC CGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCGCGC3CAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCC3CAGCC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGAT3TG CGAG3GCCC CGCGTTCCGC CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
CTG CTG TTC TCC TGC TCC GTC GGC CGT GGC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
GTC AAC ATT GGC GCG GTG CTG AGC ACC CGC AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
CGC GAG GCC GTG AAC CAG GGC AAC AAG CGC CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
CAG CTC AAT GCC ACC TCC GTC ACC CAC AAG CCC AAC GGC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAC GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
GTC TCC TAC ACA GGC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

																	175																		181																		185																																			
CCT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG		867																																																																							
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys																																																																									
																	190																		195																		200																																			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC		915																																																																							
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val																																																																									
																	205																		210																		215																																			
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA		963																																																																							
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala																																																																									
																	220																		225																		230																																			
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC		1011																																																																							
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly																																																																									
																	235																		240																		245																		250																	
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC		1059																																																																							
Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile																																																																									
																	255																		260																		265																																			
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC		1107																																																																							
Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser																																																																									
																	270																		275																		280																																			
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG		1155																																																																							
Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys																																																																									
																	285																		290																		295																																			
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC		1203																																																																							
Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile																																																																									
																	300																		305																		310																																			
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT		1251																																																																							
Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr																																																																									
																	315																		320																		325																		330																	
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG		1299																																																																							
Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg																																																																									
																	335																		340																		345																																			
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG		1347																																																																							
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val																																																																									
																	350																		355																		360																																			
CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG		1395																																																																							
Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys																																																																									
																	365																		370																		375																																			
ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG		1443																																																																							
Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met																																																																									
																	380																		385																		390																																			
TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC		1491																																																																							
Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr																																																																									
																	395																		400																		405																		410																	
GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	SAG	TTC	ACA	GTC		1539																																																																							
Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val																																																																									
																	415																		420																		425																																			
AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG		1587																																																																							
Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr																																																																									
																	430																		435																		440																																			

TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	1635
Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	
		445					450					455				
TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683
Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	
	460					465					470					
GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
	475				480					485					490	
AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
				495					500					505		
AGC	GGC	CAC	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
			510					515					520			
CGC	GCG	CAC	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
		525					530					535				
ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTT	1923
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
	540					545					550					
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
	555				560					565					570	
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
				575						580				585		
GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	
			590					595					600			
CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
		605					610					615				
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
	620					625					630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
	635				640					645					650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACC	GGC	2259
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655					660					665		
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCC	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
			670					675					680			
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
		685					690					695				
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
	700					705					710					

GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CCG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCCC GGAGGCGCCC ACCTGCCCCAG TTAGCCCCGGC CAAGGACACT GATGGGTCCCT	3087
GCTGCTCGGG AAGGCCTGAG GGAAGCCCCAC CCGCCCCAGA GACTGCCCCAC CCTGGGCCTC	3147
CCGTCCGT	3155

(2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 922 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met 1	Ser	Thr	Met	Arg 5	Leu	Leu	Thr	Leu	Ala 10	Leu	Leu	Phe	Ser	Cys 15	Ser
Val	Ala	Arg	Ala 20	Ala	Cys	Asp	Pro	Lys 25	Ile	Val	Asn	Ile	Gly 30	Ala	Val
Leu	Ser	Thr 35	Arg	Lys	His	Glu	Gln 40	Met	Phe	Arg	Glu	Ala 45	Val	Asn	Gln
Ala	Asn 50	Lys	Arg	His	Gly	Ser 55	Trp	Lys	Ile	Gln	Leu 60	Asn	Ala	Thr	Ser
Val 65	Thr	His	Lys	Pro	Asn 70	Ala	Ile	Gln	Met	Ala 75	Leu	Ser	Val	Cys	Glu 80
Asp	Leu	Ile	Ser	Ser 85	Gln	Val	Tyr	Ala	Ile 90	Leu	Val	Ser	His	Pro 95	Pro
Thr	Pro	Asn	Asp 100	His	Phe	Thr	Pro	Thr 105	Pro	Val	Ser	Tyr	Thr 110	Ala	Gly
Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr	Thr	Arg	Met 125	Ser	Ile	Tyr
Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu	Arg	Thr 140	Val	Pro	Pro	Tyr
Ser 145	His	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met	Met 155	Arg	Val	Tyr	Ser	Trp 160
Asn	His	Ile	Ile	Leu 165	Leu	Val	Ser	Asp	Asp 170	His	Glu	Gly	Arg	Ala 175	Ala
Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu 185	Glu	Arg	Glu	Ser	Lys 190	Ala	Glu
Lys	Val	Leu 195	Gln	Phe	Asp	Pro	Gly 200	Thr	Lys	Asn	Val	Thr 205	Ala	Leu	Leu
Met	Glu 210	Ala	Lys	Glu	Leu	Glu 215	Ala	Arg	Val	Ile	Ile 220	Leu	Ser	Ala	Ser
Glu 225	Asp	Asp	Ala	Ala	Thr 230	Val	Tyr	Arg	Ala	Ala 235	Ala	Met	Leu	Asn	Met 240
Thr	Gly	Ser	Gly	Tyr 245	Val	Trp	Leu	Val	Gly 250	Glu	Arg	Glu	Ile	Ser 255	Gly
Asn	Ala	Leu	Arg 260	Tyr	Ala	Pro	Asp	Gly 265	Ile	Leu	Gly	Leu	Gln 270	Leu	Ile
Asn	Gly	Lys 275	Asn	Glu	Ser	Ala	His 280	Ile	Ser	Asp	Ala 285	Val	Gly	Val	Val
Ala	Gln 290	Ala	Val	His	Glu	Leu 295	Leu	Glu	Lys	Glu	Asn 300	Ile	Thr	Asp	Pro
Pro 305	Arg	Gly	Cys	Val	Gly 310	Asn	Thr	Asn	Ile	Trp 315	Lys	Thr	Gly	Pro	Leu 320
Phe	Lys	Arg	Val	Leu 325	Met	Ser	Ser	Lys	Tyr 330	Ala	Asp	Gly	Val	Thr 335	Gly
Arg	Val	Glu	Phe 340	Asn	Glu	Asp	Gly	Asp 345	Arg	Lys	Phe	Ala 350	Asn	Tyr	Ser

Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	355	360	365	
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	370	375	380	
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	385	390	395	400
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	405	410	415	
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	420	425	430	
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	435	440	445	
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	450	455	460	
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	465	470	475	480
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	485	490	495	
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	500	505	510	
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	515	520	525	
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	530	535	540	
Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	545	550	555	560
Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	565	570	575	
Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	580	585	590	
Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	595	600	605	
Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	610	615	620	
Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	625	630	635	640
Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	645	650	655	
Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	660	665	670	
Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	675	680	685	
Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	690	695	700	

-125-

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His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
705              710              715              720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
              725              730              735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
              740              745              750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
755              760              765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
770              775              780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
785              790              795              800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
              805              810              815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
820              825              830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
835              840              845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
850              855              860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
865              870              875              880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
885              890              895

Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn
900              905              910

Leu Ser Asp Pro Ser Val Ser Thr Val Val
915              920

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2540 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME KEY: CDS
  - (B) LOCATION: 1..2334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	48
Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	
1				5				10						15		
CGT	ATA	CCC	GTG	CTG	GGG	CTG	ACC	ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	96



Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	
			20					25					30			
AAG	ASC	ATC	CAC	CTG	AGC	TTC	CTG	CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	144
Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	
		35					40					45				
CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	192
Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	Asn	His	
	50					55					60					
ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	240
Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	
65					70					75					80	
CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	288
Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	
				85					90					95		
AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	336
Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	
			100					105					110			
AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	384
Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	
		115					120					125				
GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	432
Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	
	130					135					140					
TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	480
Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	
145					150					155					160	
CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	528
Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	
				165					170					175		
AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	576
Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	
		180						185					190			
GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	624
Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	
		195					200					205				
ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	TAC	AAT	GSC	672
Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	
	210					215					220					
ACC	CAC	GTG	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	720
Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	
	225					230				235					240	
ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	768
Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	
				245					250					255		
ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	816
Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	
			260					265					270			
GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	864
Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	
		275					280					285				

GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	TGG	CCG	GGC	AGC	CCC	CGC	CAC	910
Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	
290						295					300					
ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	960
Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	
305					310					315					320	
CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	1008
Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	
				325					330					335		
GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	1056
Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	
			340					345					350			
TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	1104
Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	
		355					360					365				
GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	1152
Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	
		370				375					380					
TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	1200
Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	
385					390					395					400	
ATT	CCC	CGG	AGC	ACG	CTG	GAC	TGG	TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	1248
Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	
				405					410					415		
CTG	TGG	CTG	CTG	GTG	GGG	CTG	TGG	GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	1296
Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	Leu	
				420				425					430			
TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	1344
Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	
			435				440					445				
GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	CTG	TCC	TGG	GCC	ATG	TGG	TTC	1392
Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	
			450			455					460					
TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	1440
Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	
465				470					475						480	
AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	1488
Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	
				485					490					495		
ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	1536
Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	
			500					505					510			
GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	1584
Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	
			515				520					525				
AAC	CCC	TGG	GAC	AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	ACC	TCC	GTG	1632
Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	
	530					535					540					
GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	1680
Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	
545					550					555					560	

ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCG ATC CAG GCC GTG	1728
Met Glu Lys His Asn Tyr Glu Ser Ala Glu Ala Ile Gln Ala Val	
565 570 575	
AGA GAC AAC AAG CTG CAT GCG TTC ATC TGG GAC TCG GCG GTG CTG GAG	1776
Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu	
580 585 590	
TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT	1824
Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe	
595 600 605	
TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG	1872
Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys	
610 615 620	
CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG	1920
Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met	
625 630 635 640	
GAA GAC CTG GAC AAG ACG TGG GTT CCG TAT CAG GAA TGT GAC TCG CGC	1968
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
645 650 655	
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC	2016
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
660 665 670	
ATG CTG GTA GCT GGG GGC ATC GTG GCG GGG ATC TTC CTG ATT TTC ATC	2064
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
675 680 685	
GAG ATT GCC TAC AAG CCG CAC AAG GAT GCT CGC CCG AAG CAG ATG CAG	2112
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
690 695 700	
CTG GCC TTT GCC GCC GTT AAC GTG TGG CCG AAG AAC CTG CAG GAT AGA	2160
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
705 710 715 720	
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG	2208
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
725 730 735	
GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC	2256
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
740 745 750	
AAA GAC ACG CAG TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC	2304
Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu	
755 760 765	
TCA GAT CCC TCG GTC AGC ACC GTG GTG TGAGGCCCGG GAGGGCGCCC	2351
Ser Asp Pro Ser Val Ser Thr Val Val	
770 775	
ACCTGCCCGAG TTAGCCCGGG CAAGGACACT GATGGGTCTT GCTGCTCGGG AAGGCCTGAG	2411
GGAAGCCCGAC CCGCCCGAGA GACTGCCCGAC COTGGGCGCTC CCCTCCCTCC GCCCGCCCGAC	2471
CCCGCTGCCT GCGGGGCAGC CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG	2531
GGGCAGAGC	2540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	1	5	10	15
Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	20	25	30	
Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	35	40	45	
Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	Asn	His	50	55	60	
Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	65	70	75	80
Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	85	90	95	
Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	100	105	110	
Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	115	120	125	
Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	130	135	140	
Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	145	150	155	160
Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	165	170	175	
Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	180	185	190	
Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	195	200	205	
Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	210	215	220	
Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	225	230	235	240
Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	245	250	255	
Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	260	265	270	
Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	275	280	285	
Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	290	295	300	
Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys				

305		310		315		320
Leu Ala Arg Thr Met	Asn Phe Thr Tyr Glu	Val His Leu Val Ala Asp				
	325		330			335
Gly Lys Phe Gly Thr Gln Glu Arg	Val Asn Asn Ser Asn Lys Lys Glu					
	340		345			350
Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile						
	355		360			365
Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe						
	370		375			380
Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu						
	385		390			395
Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr						
	405		410			415
Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu						
	420		425			430
Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser						
	435		440			445
Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe						
	450		455			460
Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg						
	465		470			475
Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met						
	485		490			495
Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu						
	500		505			510
Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg						
	515		520			525
Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val						
	530		535			540
Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His						
	545		550			555
Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val						
	565		570			575
Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu						
	580		585			590
Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe						
	595		600			605
Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys						
	610		615			620
Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met						
	625		630			635
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg						
	645		650			655
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe						

660	665	670
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile		
675	680	685
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln		
690	695	700
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg		
705	710	715
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg		
725	730	735
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser		
740	745	750
Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu		
755	760	765
Ser Asp Pro Ser Val Ser Thr Val Val		
770	775	

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC	48
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1 5 10 15	
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC	96
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20 25 30	
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC	144
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35 40 45	
GAG ATT GCC TAC AAG CCG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG	192
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50 55 60	
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA	240
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65 70 75 80	
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG	288
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
85 90 95	

GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC	336
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG	384
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT	432
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG	480
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	
CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT	528
Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly	
165 170 175	
GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA	583
Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	
180 185 190	
AGGAATGTCA CG	595

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1 5 10 15	
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20 25 30	
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35 40 45	
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50 55 60	
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65 70 75 80	
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
85 90 95	
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	

Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly  
165 170 175

Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp  
180 185 190

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC3CGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGGC CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	1 5 10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Cys Asp Pro Lys Ile	15 20 25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	30 35 40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	45 50 55
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	60 65 70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	75 80 85 90
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	95 100 105
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	110 115 120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	



125				130				135								
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
140						145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	
			190					195					200			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
			205				210					215				
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
220						225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	
235					240					245					250	
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059
Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	
				255					260					265		
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107
Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	
			270					275					280			
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155
Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	
			285				290					295				
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC	1203
Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	
300						305					310					
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251
Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	
315					320					325					330	
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299
Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	
				335				340						345		
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	
			350					355					360			
CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	1395
Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	
			365				370					375				
ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443
Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	
380						385					390					

TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491
Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	
395					400					405					410	
GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539
Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	
				415					420						425	
AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	1587
Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	
			430					435							440	
TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	1635
Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	
		445					450					455				
TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683
Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	
	460					465					470					
GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
475					480					485					490	
AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
				495					500					505		
AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
			510					515					520			
CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
		525					530					535				
ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
	540					545					550					
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
555					560					565					570	
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
				575					580					585		
GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	
			590					595					600			
CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
		605					610					615				
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
	620					625					630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
635					640					645					650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655					660						665	

ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCCC GGAAGCCGCC ACCTGCCCCAG TTAGCCCGGC CAAGGACACT GATGGGTCCT	3087
GCTGCTCGGG AAGCCCTGAG GGAAGCCCCAC CCGCCCCAGA GACTGCCCCAC CCTGGGGCTC	3147

CCGTCCGTCC GCCCCCCCAC CCGCTGCTCT GGGGGGAGC CCCTGTGGA CCAAGGTGCG 3207  
 GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG GGCAGGGCCG CAGGGCGCTC 3267  
 CGGCAGAGGC AGGCCCCCTGG GGTCTCTGAG CAGTGGGGAG CGGGGGCTAA CTGCCCCCAG 3327  
 GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC CGCAGCACCA GCCTGAGCCA 3387  
 CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCGCCCCCTCC TCGGGCGCCT GCGCTCCTCT 3447  
 GCAGCCTGAG CTCCACCCTC CCCTCTTCTT GCGGCACCGC CCACCAAACA CCCCCTCTGC 3507  
 CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC ACGGCCGTCC CTGACTTCCC 3567  
 AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA GAATCGAGAG GGCTGAGCCC 3627  
 CTCCTCTCCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC CCCGGGGGTC CCCGGACGCT 3687  
 GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA CGGGAGAGCG CCACCCGCCC 3747  
 GCCCCCGCCC TCGCTCCGGG TCGGTGACCG GCCCGCCACC TTGTACAGAA CCAGCACTCC 3807  
 CAGGGCCCCA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT CTGCCCCCTCC GTCCCCAGGG 3867  
 TGCAGGCGCG CACCGCCCCA CCCCCACCTC CCGGTGTATG CAGTGGTGAT GCCTAAAGGA 3927  
 ATGTCACG 3935

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser  
 1 5 10 15  
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val  
 20 25 30  
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
 35 40 45  
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
 50 55 60  
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
 65 70 75 80  
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
 85 90 95  
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
 100 105 110  
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
 115 120 125  
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
 130 135 140

Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
145					150					155					160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
				165					170					175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu
			180					185					190		
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu
		195					200					205			
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser
	210					215					220				
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met
225					230					235					240
Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly
				245					250					255	
Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile
			260					265					270		
Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val
		275					280					285			
Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro
	290					295					300				
Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu
305					310					315					320
Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly
				325					330					335	
Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser
			340					345					350		
Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn
		355					360					365			
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly
	370					375					380				
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile
385					390					395					400
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser
				405				410						415	
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys
			420					425					430		
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg
		435					440					445			
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile
	450					455					460				
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala
465					470					475					480
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys
				485					490					495	
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met

500					505					510					
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu
	515						520					525			
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys
	530					535					540				
Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser
	545					550					555				560
Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met
				565					570					575	
Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn
			580					585					590		
Ser	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	
		595				600					605				
Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro
	610					615					620				
Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala
	625					630					635				640
Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val
				645					650					655	
Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu
			660					665					670		
Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser
		675					680					685			
Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg
	690					695					700				
His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala
	705					710					715				720
Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu
				725					730					735	
Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu
			740					745					750		
Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp
		755					760					765			
Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe
	770					775					780				
Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser
	785					790					795				800
Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val
				805					810					815	
Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe
			820					825					830		
Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met
		835					840					845			
Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp

850	855	860
Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe		
865	870	875 880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser		
	885	890 895
Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn		
	900	905 910
Leu Ser Asp Pro Ser Val Ser Thr Val Val		
915	920	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	1 5 10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	15 20 25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	30 35 40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	45 50 55
CAG CTC AAT GGC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	60 65 70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	75 80 85 90
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579

Leu	Val	Ser	His	Pro 95	Pro	Thr	Pro	Asn	Asp 100	His	Phe	Thr	Pro	Thr 105	Pro		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627	
Val	Ser	Tyr	Thr 110	Ala	Gly	Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr		
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675	
Thr	Arg	Met 125	Ser	Ile	Tyr	Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu		
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723	
Arg	Thr	Val 140	Pro	Pro	Tyr	Ser	His 145	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met		
ATG	CGT	GTG	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771	
Met	Arg	Val 155	Tyr	Ser	Trp 160	Asn	His	Ile	Ile	Leu 165	Leu	Val	Ser	Asp	Asp 170		
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819	
His	Glu	Gly	Arg 175	Ala	Ala	Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu	Glu 185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867	
Arg	Glu	Ser 190	Lys	Ala	Glu	Lys	Val 195	Leu	Gln	Phe	Asp	Pro 200	Gly	Thr	Lys		
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915	
Asn	Val	Thr 205	Ala	Leu	Leu	Met	Glu 210	Ala	Lys	Glu	Leu 215	Glu	Ala	Arg	Val		
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963	
Ile	Ile	Leu 220	Ser	Ala	Ser	Glu 225	Asp	Asp	Ala	Ala	Thr 230	Val	Tyr	Arg	Ala		
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC	1011	
Ala	Ala	Met	Leu	Asn	Met 240	Thr	Gly	Ser	Gly 245	Tyr	Val	Trp	Leu	Val	Gly 250		
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059	
Glu	Arg	Glu	Ile 255	Ser	Gly	Asn	Ala	Leu	Arg 260	Tyr	Ala	Pro	Asp	Gly 265	Ile		
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107	
Leu	Gly	Leu 270	Gln	Leu	Ile	Asn	Gly 275	Lys	Asn	Glu	Ser	Ala 280	His	Ile	Ser		
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155	
Asp	Ala	Val 285	Gly	Val	Val	Ala	Gln 290	Ala	Val	His	Glu	Leu 295	Leu	Glu	Lys		
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC	1203	
Glu	Asn	Ile 300	Thr	Asp	Pro	Pro	Arg 305	Gly	Cys	Val	Gly 310	Asn	Thr	Asn	Ile		
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251	
Trp	Lys	Thr 315	Gly	Pro	Leu 320	Phe	Lys	Arg	Val 325	Met	Ser	Ser	Lys	Tyr 330			
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299	
Ala	Asp	Gly	Val 335	Thr	Gly	Arg	Val 340	Glu	Phe	Asn	Glu	Asp	Gly 345	Arg			
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347	
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val		



2153

Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
620						625					630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
635					640					645					650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GCG	2259
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655					660					665		
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
			670					675					680			
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
		685					690					695				
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
	700					705					710					
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTG	ATC	2451
Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	
715					720					725					730	
TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	
				735					740					745		
GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GCG	TTC	GCG	ATA	GCG	ATG	2547
Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	
			750					755					760			
CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG	2595
Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	
		765					770					775				
TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG	2643
Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	
		780				785					790					
TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT	2691
Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	
795					800					805					810	
GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	2739
Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	
				815					820					825		
GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	2787
Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	
			830					835					840			
GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	2835
Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	
			845				850					855				
CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	2883
Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	
		860				865					870					
AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	2931
Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	
875					880					885					890	

TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT	2979
Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu	
895 900 905	
CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC	3027
Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro	
910 915 920	
CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC	3075
Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr	
925 930 935	
AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT	3123
Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala	
940 945 950	
CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC	3171
Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr	
955 960 965 970	
TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG	3211
Ser Arg Cys Met Gln Trp	
975	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	

165										170					175				
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu				
			180					185					190						
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu				
		195					200					205							
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser				
	210					215					220								
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met				
225					230				235						240				
Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly				
			245						250					255					
Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile				
			260					265					270						
Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val				
		275					280					285							
Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro				
	290					295					300								
Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu				
305					310					315					320				
Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly				
			325						330					335					
Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser				
			340					345					350						
Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn				
	355						360					365							
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly				
	370					375					380								
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile				
385					390					395					400				
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser				
			405						410					415					
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys				
			420					425					430						
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg				
	435						440					445							
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile				
	450				455						460								
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala				
465					470					475					480				
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys				
			485						490					495					
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met				
		500						505					510						
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu				

515					520					525					
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys
530					535					540					
Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser
545					550					555					560
Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met
				565					570					575	
Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn
			580					585					590		
Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp
			595				600					605			
Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro
610					615					620					
Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala
625					630					635					640
Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val
				645					650					655	
Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu
			660					665					670		
Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser
		675					680					685			
Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg
	690					695					700				
His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala
705					710					715					720
Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu
			725						730					735	
Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu
			740					745					750		
Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp
		755					760					765			
Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe
	770					775					780				
Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser
785					790					795					800
Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val
				805					810					815	
Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe
			820					825					830		
Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met
		835					840					845			
Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp
	850					855					860				
Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe

865	870	875	880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser	885	890	895
Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro	900	905	910
Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val	915	920	925
Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg	930	935	940
Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln	945	950	955
Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	965	970	975

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4361 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 262..3141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	1 5 10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	15 20 25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	30 35 40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	45 50 55

CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
60						65					70					
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
75					80					85					90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCT	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
235					240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
				255					260					265		
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
			270					275					280			
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
		285					290					295				
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
	300					305					310					
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
315					320					325					330	

GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG	1299
Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu	
335 340 345	
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT	1347
Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn	
350 355 360	
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG	1395
Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln	
365 370 375	
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC	1443
Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile	
380 385 390	
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT	1491
Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro	
395 400 405 410	
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG	1539
Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln	
415 420 425	
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG	1587
Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys	
430 435 440	
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC	1635
Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr	
445 450 455	
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG	1683
Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln	
460 465 470	
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC	1731
Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr	
475 480 485 490	
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC	1779
Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly	
495 500 505	
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG	1827
Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met	
510 515 520	
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA	1875
Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu	
525 530 535	
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC	1923
Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe	
540 545 550	
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC	1971
Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser	
555 560 565 570	
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG	2019
Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu	
575 580 585	
GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC	2067
Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp	
590 595 600	



CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	
		605					610					615				
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	
	620					625					630					
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
635					640					645					650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660					665		
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
		670						675					680			
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
		685					690					695				
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
	700					705					710					
CGC	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	2451
Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	
715					720					725					730	
AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	2499
Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	
				735					740					745		
CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	2547
Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	
			750					755					760			
CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	2595
Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	
		765					770					775				
TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	2643
Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	
	780					785					790					
CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	2691
Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	
795					800					805					810	
AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	2739
Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	
				815					820					825		
GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	2787
Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	
			830					835					840			
GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	2835
Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	
		845					850					855				
AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	2883
Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	
	860					865					870					

GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser 910 915 920	3027
ACC GGG GGT GGA CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu 925 930 935	3075
CCG CGA CGC GCT ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser 940 945 950	3123
CGT CAT AGG GAG AGC TGAGACTCCC CGCCCCGCCCT CCTCTGCCCC CTCCCCCGCA Arg His Arg Glu Ser 960	3178
GACAGACAGA CAGACGGACG GGACAGCGGC CCGGCCACAG CAGAGCCCCG GAGCACCACG	3238
GGGTGCGGGG AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG	3298
CCGGCTGGCC GGTCCACCCC GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGTAAACGGG	3358
CGCCTTGTCT GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC ACBBBCCCGC	3418
TCAACCTCTC AGATCCCTCC GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CCCCCACCTC	3478
CCCAGTTAGC CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAZ	3538
CCCACCCGCC CCAGAGACTC CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCAACCCCGC	3598
TGCCTGGCGG GCAGCCCTTC CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA	3658
GAGCTGAGTC GGCTGGGGAG GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT	3718
CTGAGCAGTG GGGAGCGGGG GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG	3778
CAGCCCCATC CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG	3838
CTGGGTGCGC CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCTTC	3898
TTCTTGCGGC ACCGCCACCC AAACACCCCG TCTGCCCTT GACGCCACAC GCGGGGGTGG	3958
GCGCTGCCCT CCCCCACGGC CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCCCTC	4018
GGGCCGCCTC CTCAGAAATC GAGAGGGCTG AGCCCTCCT CTCTCTGTCC GGCCTGCAGC	4078
ACAGAAGGGG CCTCCCCCGG GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCTTGC	4138
CCTGCACCTT GGGCACGGGA GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCCT	4198
GACCGGCCCG CCACCTTSTA CAGAACCAGC ACTCCAGGG CCGAGCGCG TGCCTTCCCC	4258
GTGCGCAGCC GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCAAACCCCC	4318
ACCTCCCGGT STATGCAGTG GTGATGCCTA AAGGAATGTC ACG	4361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met 1	Ser	Thr	Met	Arg 5	Leu	Leu	Thr	Leu	Ala 10	Leu	Leu	Phe	Ser	Cys 15	Ser
Val	Ala	Arg	Ala 20	Ala	Cys	Asp	Pro	Lys 25	Ile	Val	Asn	Ile	Gly 30	Ala	Val
Leu	Ser	Thr 35	Arg	Lys	His	Glu	Gln 40	Met	Phe	Arg	Glu	Ala 45	Val	Asn	Gln
Ala	Asn 50	Lys	Arg	His	Gly	Ser 55	Trp	Lys	Ile	Gln	Leu 60	Asn	Ala	Thr	Ser
Val 65	Thr	His	Lys	Pro	Asn 70	Ala	Ile	Gln	Met	Ala 75	Leu	Ser	Val	Cys	Glu 80
Asp	Leu	Ile	Ser	Ser 85	Gln	Val	Tyr	Ala	Ile 90	Leu	Val	Ser	His	Pro 95	Pro
Thr	Pro	Asn	Asp 100	His	Phe	Thr	Pro	Thr 105	Pro	Val	Ser	Tyr	Thr 110	Ala	Gly
Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr	Thr	Arg	Met 125	Ser	Ile	Tyr
Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu	Arg	Thr 140	Val	Pro	Pro	Tyr
Ser 145	His	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met	Met 155	Arg	Val	Tyr	Ser	Trp 160
Asn	His	Ile	Ile	Leu 165	Leu	Val	Ser	Asp	Asp 170	His	Glu	Gly	Arg	Ala 175	Ala
Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu 185	Glu	Arg	Glu	Ser	Lys 190	Ser	Lys
Lys	Arg	Asn 195	Tyr	Glu	Asn	Leu	Asp 200	Gln	Leu	Ser	Tyr	Asp 205	Asn	Lys	Arg
Gly	Pro 210	Lys	Ala	Glu	Lys	Val 215	Leu	Gln	Phe	Asp	Pro 220	Gly	Thr	Lys	Asn
Val 225	Thr	Ala	Leu	Leu	Met 230	Glu	Ala	Lys	Glu	Leu 235	Glu	Ala	Arg	Val	Ile 240
Ile	Leu	Ser	Ala	Ser 245	Glu	Asp	Asp	Ala	Ala 250	Thr	Val	Tyr	Arg	Ala 255	Ala
Ala	Met	Leu	Asn 260	Met	Thr	Gly	Ser	Gly 265	Tyr	Val	Trp	Leu	Val	Gly 270	Glu
Arg	Glu	Ile 275	Ser	Gly	Asn	Ala	Leu 280	Arg	Tyr	Ala	Pro	Asp 285	Gly	Ile	Leu
Gly	Leu 290	Gln	Leu	Ile	Asn	Gly 295	Lys	Asn	Glu	Ser	Ala 300	His	Ile	Ser	Asp
Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu

305		310		315		320
Asn Ile Thr Asp	Pro 325	Pro Arg Gly Cys Val 330	Gly Asn Thr Asn Ile Trp 335			
Lys Thr Gly	Pro 340	Leu Phe Lys Arg Val 345	Leu Met Ser Ser Lys Tyr Ala 350			
Asp Gly Val 355	Thr Gly Arg Val 360	Glu Phe Asn Glu Asp 365	Gly Asp Arg Lys			
Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln 370 375 380						
Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile 385 390 395 400						
Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser 405 410 415						
Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val 420 425 430						
Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn 435 440 445						
Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser 450 455 460						
Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys 465 470 475 480						
Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu 485 490 495						
Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn 500 505 510						
Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser 515 520 525						
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg 530 535 540						
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr 545 550 555 560						
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met 565 570 575						
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His 580 585 590						
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly 595 600 605						
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu 610 615 620						
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile 625 630 635 640						
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val 645 650 655						
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu						

660	665	670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile 675 680 685		
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr 690 695 700		
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu 705 710 715 720		
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala 725 730 735		
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp 740 745 750		
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val 755 760 765		
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg 770 775 780		
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser 785 790 795 800		
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr 805 810 815		
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu 820 825 830		
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly 835 840 845		
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala 850 855 860		
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg 865 870 875 880		
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys 885 890 895		
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe 900 905 910		
Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly 915 920 925		
Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu 930 935 940		
Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 945 950 955		

(2) INFORMATION FOR SEQ ID NO:25:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(11) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCDBACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGAGCC CGCGGGGGCCG GGCBSAGCSA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGGGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG	867
Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	200
190 195	

TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
235					240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
			270					275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
	300					305					310					
GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
315					320					325					330	
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
			335				340							345		
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
			350				355					360				
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
		365					370					375				
GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
	380					385					390					
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
				400						405					410	
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415					420					425		
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
			430					435				440				
GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	1635
Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	
		445					450					455				
CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	1683
Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	
		460				465					470					

GAG Glu 475	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile 480	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro 485	TTC Phe	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 490	1731
CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val 495	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro 500	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp 505	TCG Ser	1779
TTC Phe	ATG Met	CAG Gln	CCG Pro 510	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu 515	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly 520	CTG Leu	TCG Ser	1827
GTG Val	CAC His	GTG Val	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg	TTC Phe	AGC Ser	CCC Pro	1875
TTC Phe	GGC Gly 540	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn 545	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala	CTG Leu	1923
ACC Thr 555	CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met 560	TGG Trp	TTC Phe	TCC Ser	TGG Trp	GGC Gly 565	GTC Val	CTG Leu	CTC Leu	AAC Asn	TCC Ser 570	1971
GGC Gly	ATC Ile	GCG Gly	GAA Glu	GGC Gly 575	GCC Ala	CCC Pro	AGA Arg	AGC Ser	TTC Phe	TCA Ser	GCG Ala	CGC Arg	ATC Ile	CTG Leu	GGC Gly 585	2019
ATG Met	GTG Val	TGG Trp	GCC Ala 590	GGC Gly	TTT Phe	GCC Ala	ATG Met	ATC Ile 595	ATC Ile	GTG Val	GCC Ala	TCC Ser	TAC Tyr 600	ACC Thr	GCC Ala	2067
AAC Asn	CTG Leu	GCG Ala	GCC Ala	TTC Phe	CTG Leu	GTG Val	CTG Leu	GAC Asp	CGG Arg	CCG Pro	GAG Glu	GAG Glu	CGC Arg	ATC Ile	ACG Thr	2115
GGC Gly 620	ATC Ile	AAC Asn	GAC Asp	CCT Pro	CGG Arg	CTG Leu 625	AGG Arg	AAC Asn	CCC Pro	TCG Ser	GAC Asp 630	AAG Lys	TTT Phe	ATC Ile	TAC Tyr	2163
GCC Ala 635	ACG Thr	GTG Val	AAG Lys	CAG Gln	AGC Ser 640	TCC Ser	GTG Val	GAT Asp	ATC Ile	TAC Tyr 645	TTC Phe	CGG Arg	CGC Arg	CAG Gln	GTG Val 650	2211
GAG Glu	CTG Leu	AGC Ser	ACC Thr	ATG Met 655	TAC Tyr	CGG Arg	CAT His	ATG Met	GAG Glu 660	AAG Lys	CAC His	AAC Asn	TAC Tyr	GAG Glu 665	AGT Ser	2259
GCG Ala	GCG Ala	GAG Glu	GCC Ile 670	ATC Ile	CAG Gln	GCC Ala	GTG Val	AGA Arg 675	GAC Asp	AAC Asn	AAG Lys	CTG Leu	CAT His	GCC Ala 680	TTC Phe	2307
ATC Ile	TGG Trp	GAC Asp 685	TCG Ser	GCG Ala	GTG Val	CTG Leu	GAG Glu 690	TTC Phe	GAG Glu	GCC Ala	TCG Ser	CAG Gln	AAG Lys	TGC Cys	GAC Asp	2355
CTG Leu 700	GTG Val	ACG Thr	ACT Thr	GGA Gly	GAG Glu	CTG Leu 705	TTT Phe	TTC Phe	CGC Arg	TCG Ser	GGC Gly 710	TTC Phe	GGC Gly	ATA Ile	GGC Gly	2403
ATG Met 715	CGC Arg	AAA Lys	GAC Asp	AGC Ser	CCC Pro 720	TGG Trp	AAG Lys	CAG Gln	AAC Asn	GTG Val 725	TCC Ser	CTG Leu	TCC Ser	ATC Ile	CTC Leu 730	2451
AAG Lys	TCC Ser	CAC His	GAG Glu	AAT Asn 735	GGC Gly	TTC Phe	ATG Met	GAA Glu	GAC Asp 740	CTG Leu	GAC Asp	AAG Lys	ACG Thr	TGG Trp 745	GTT Val	2499



CCG TAT CAG GAA TGT GAT TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT	2547
Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr	
750 755 760	
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG	2595
Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val	
765 770 775	
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG	2643
Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys	
780 785 790	
GAT GGT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG	2691
Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val	
795 800 805 810	
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC	2739
Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp	
815 820 825	
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC	2787
Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser	
830 835 840	
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA	2835
Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly	
845 850 855	
CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT	2883
Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala	
860 865 870	
ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG	2931
Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu	
875 880 885 890	
AGC TGAGACTCCC CGCCCCGCCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA	2984
Ser	
CAGACGACG GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG	3044
AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC	3104
GGTCCACCCC GTCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTCTCT	3164
GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCG TCAACCTCTC	3224
AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCACCTG CCCAGTTAGC	3284
CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC	3344
CCAGAGACTG CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCTTGCGG	3404
GCAGCCCTCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC	3464
GGCTG33GAG GGCCGCGAGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG	3524
GGGAGCGGGG GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC	3584
CTTCCGCGAG CAGCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTGCGC	3644
CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCTCT TTCTTGCGGC	3704
ACCGCCCAAC AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCCTGCGCCT	3764
CCCCACGCG CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCTC GGGCCGCTC	3824

CTCCAGAATC GAGAGGGCTG ABBCCCTCCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG	3884
GCCTCCCCGG GGGTCCCCGG ABBCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT	3944
GGGCACGGGA GAGCGCCACC CGCCCCCCCC CGCCCTCGCT CCGGGTGCCT GACCGGCCCCG	4004
CCACCTTGTA CAGAACCAGG ACTCCCAGGG CCGAGCGCG TGCCTTCCCC GTGCGCAGCC	4064
GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT	4124
GTATGCAGTG GTGATGCCTA AAGGAATGTC ACG	4157

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	1	5	10	15
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	20	25	30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln	35	40	45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser	50	55	60	
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu	65	70	75	80
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro	85	90	95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	100	105	110	
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	115	120	125	
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	130	135	140	
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	145	150	155	160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	165	170	175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	180	185	190	
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	195	200	205	
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	210	215	220	
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile				

225		230		235		240
Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala	245	250	255			
Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro	260	265	270			
Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr	275	280	285			
Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr	290	295	300			
Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr	305	310	315			320
Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly	325	330	335			
Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys	340	345	350			
Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu	355	360	365			
Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val	370	375	380			
Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro	385	390	395			400
Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu	405	410	415			
Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val	420	425	430			
Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys	435	440	445			
Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp	450	455	460			
Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile	465	470	475			480
Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys	485	490	495			
Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln	500	505	510			
Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val	515	520	525			
Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val	530	535	540			
Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met	545	550	555			560
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala	565	570	575			
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe						

580					585					590				
Ala Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu
595					600					605				
Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro
610					615					620				
Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln
625					630					635				640
Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met
				645					650					655
Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile
			660					665					670	Gln
Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala
			675				680					685		Val
Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly
	690					695					700			Glu
Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser
705					710					715				720
Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn
				725					730					735
Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys
			740					745					750	Asp
Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala
				755				760					765	Gly
Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu
	770					775					780			Ile
Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys
785					790					795				Gln
Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu
				805					810					815
Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala
			820					825					830	Thr
Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg
				835				840					845	
Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln
	850					855					860			Asn
Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu
865						870					875			Gly
Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser				
				885					890					

(2) INFORMATION FOR SEQ ID NO:27:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3794 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both

(D) TOPOLOGY: both

(12) MOLECULE TYPE: cDNA

(13) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAAGCGGGG	GTTCGGAGCT	GTGCCCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG	60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC	120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGGCCG	GGCGAGCGCA	180
GGACGGCCCCG	GAAGCCCCCG	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG	240
CCAGGCCCCGC	GGCCCCGAGCC	C	ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC			291
			Met Ser Thr Met Arg	Leu Leu Thr Leu Ala		
			1 5		10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC						339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile						
			15 20		25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC						387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe						
			30 35		40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT						435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile						
			45 50		55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG						483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met						
			60 65		70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC						531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile						
			75 80		85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT						579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro						
			95 100		105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC						627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr						
			110 115		120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG						675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu						
			125 130		135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG						723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met						
			140 145		150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC						771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp						
			155 160		165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG						819

His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
		220				225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
		235			240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
			270					275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
		300				305					310					
GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
		315			320					325					330	
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
				335					340					345		
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
			350					355					360			
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
		365					370					375				
GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
		380				385					390					
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
					400					405					410	
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415					420					425		
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
			430					435					440			

GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	1635
Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	
		445					450					455				
CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	1683
Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	
		460				465					470					
GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	1731
Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	
		475			480					485					490	
CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	1779
Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	
				495					500					505		
TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	1827
Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	
			510					515					520			
GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	1875
Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	
		525					530					535				
TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	1923
Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	
		540				545					550					
ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	1971
Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	
		555			560					565					570	
GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	2019
Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	
				575					580					585		
ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	2067
Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	
			590					595					600			
AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	2115
Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	
		605					610					615				
GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	2163
Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	
		620				625					630					
GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	2211
Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	
					640					645					650	
GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	2259
Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	
				655					660					665		
GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	2307
Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	
			670					675					680			
ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	2355
Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	
		685					690					695				
CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	2403
Leu	Val	Thr	Thr	Gly	Glu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly		
		700				705					710					

ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC	2451
Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu	
715 720 725 730	
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT	2499
Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val	
735 740 745	
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT	2547
Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr	
750 755 760	
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG	2595
Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val	
765 770 775	
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG	2643
Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys	
780 785 790	
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG	2691
Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val	
795 800 805 810	
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC	2739
Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp	
815 820 825	
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC	2787
Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser	
830 835 840	
AGC TTC AAG AAG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT	2835
Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr	
845 850 855	
GAT ATC ACG GGC CCC CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG	2883
Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val	
860 865 870	
GTG TGAGGCCCCC GGAGGCGCCC ACCTGCCCAG TTAGCCCCGGC CAAGGACACT	2936
Val	
875	
GATGGGTCCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCAC	2996
CCTGGGCCTC CCGTCCGTCC GCCCGCCCAC CCCGCTGCCT GGCGGGCAGC CCCTGCTGGA	3056
CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGCTG GGCAGGGCCG	3116
CAGGGCGCTC CGGCAGAGGC AGGCCCCCTGG GGTCTCTGAG CAGTGGGGAG CCGGGGCTAA	3176
CTGCCCCCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC CGCAGCACCA	3236
GCCTGAGCCA CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCGCCCCCTCC TCGGGC3CCT	3296
GCGCTCCTCT GCAGCCTGAG CTCCACCCTC CCCTCTTCTT GCGGCACCGC CCACCAAACA	3356
CCCCGTCTGC CCCTTGACGC CACACGCGCG GGCTGGCGCT GCCCTCCCCC ACGGCGCTCC	3416
CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA GAATCGAGAG	3476
GGCTGAGCCC CTCTCTCTCT CGTCCGGCCT GCAGCACAGA AGGGGGGCTC CCGGGGGCTC	3536
CCCGGACGCT GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA CCGGAGAGCG	3596
CCACCCGCCC GCCCCCGCCC TCGCTCCGGG TCGGTGACCG GCCCGCCACC TTGTACAGAA	3656



CCAGCACTCC CAGGGCCCCGA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT CTGCCCCCTCC	3716
GTCCCCAGGG TGCAGGCGCG CACCGCCCCAA CCCCCACCTC CCGGTGTATG CAGTGGTGAT	3776
GCCTAAAGGA ATGTCACG	3794

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
	20							25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
		35					40					45			
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50					55					60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65				70				75					80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
			85						90					95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
		100						105					110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
	115						120					125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
	130					135					140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
	145				150				155					160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
			165					170						175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys
		180						185					190		
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg
	195						200					205			
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn
	210				215						220				
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile
	225				230					235				240	
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala
			245					250						255	
Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro

260					265					270					
Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr
		275					280					285			
Gly	Arg	Val	Glu	Phe	Asn	Gln	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr
	290					295					300				
Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr
	305					310					315				320
Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly
				325					330					335	
Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys
				340					345					350	
Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu
				355					360					365	
Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val
		370					375					380			
Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro
				390								395			400
Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu
				405					410					415	
Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val
				420					425					430	
Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys
		435					440					445			
Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp
		450					455					460			
Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile
				470							475				480
Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys
				485					490					495	
Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln
				500				505					510		
Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val
				515			520					525			
Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val
				530			535					540			
Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met
				550							555				560
Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala
				565					570					575	
Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe
				580				585					590		
Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu
				595			600					605			
Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg
				610			615				620				

Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	625	630	635	640
Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	645	650	655	
Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	660	665	670	
Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	675	680	685	
Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	690	695	700	
Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	705	710	715	720
Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	725	730	735	
Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	740	745	750	
Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	755	760	765	
Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	770	775	780	
Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	785	790	795	800
Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	805	810	815	
Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	820	825	830	
Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg	835	840	845	
Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro	Leu	850	855	860	
Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val						865	870	875	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGG3CTG AGCGCCGAGC CCCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGG3G GAGACGTGGC GTCCGCAGCC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCC3C GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	
205 210 215	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA	963
Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	
220 225 230	

GCC Ala 235	GCG Ala	ATG Met	CTG Leu	AAC Asn	ATG Met 240	ACG Thr	GGC Gly	AAC Asn	ACC Thr	AAC Asn 245	ATC Ile	TGG Trp	AAG Lys	ACC Thr	GGG Gly 250	1011
CCG Pro	CTC Leu	TTC Phe	AAG Lys	AGA Arg 255	GTG Val	CTG Leu	ATG Met	TCT Ser	TCC Ser 260	AAG Lys	TAT Tyr	GCG Ala	GAT Asp	GGG Gly 265	GTG Val	1059
ACT Thr	GGT Gly	CGC Arg	GTG Val 270	GAG Glu	TTC Phe	AAT Asn	GAG Glu	GAT Asp 275	GGG Gly	GAC Asp	CGG Arg	AAG Lys	TTC Phe 280	GCC Ala	AAC Asn	1107
TAC Tyr	AGC Ser	ATC Ile 285	ATG Met	AAC Asn	CTG Leu	CAG Gln	AAC Asn 290	CGC Arg	AAG Lys	CTG Leu	GTG Val	CAA Gln 295	GTG Val	GGC Gly	ATC Ile	1155
TAC Tyr 300	AAT Asn	GGC Gly	ACC Thr	CAC His	GTC Val	ATC Ile 305	CCT Pro	AAT Asn	GAC Asp	AGG Arg	AAG Lys 310	ATC Ile	ATC Ile	TGG Trp	CCA Pro	1203
GGC Gly 315	GGA Gly	GAG Glu	ACA Thr	GAG Glu	AAG Lys 320	CCT Pro	CGA Arg	GGG Gly	TAC Tyr	CAG Gln 325	ATG Met	TCC Ser	ACC Thr	AGA Arg	CTG Leu 330	1251
AAG Lys	ATT Ile	GTG Val	ACG Thr	ATC Ile 335	CAC His	CAG Gln	GAG Glu	CCC Pro	TTC Phe 340	GTG Val	TAC Tyr	GTC Val	AAG Lys	CCC Pro 345	ACG Thr	1299
CTG Leu	AGT Ser	GAT Asp	GGG Gly 350	ACA Thr	TGC Cys	AAG Lys	GAG Glu	GAG Glu 355	TTC Phe	ACA Thr	GTC Val	AAC Asn 360	GGC Gly	GAC Asp	CCA Pro	1347
GTC Val	AAG Lys	AAG Lys 365	GTG Val	ATC Ile	TGC Cys	ACG Thr	GGG Gly 370	CCC Pro	AAC Asn	GAC Asp	ACG Thr	TCG Ser 375	CCG Pro	GGC Gly	AGC Ser	1395
CCC Pro 380	CGC Arg	CAC His	ACG Thr	GTG Val	CCT Pro	CAG Gln 385	TGT Cys	TGC Cys	TAC Tyr	GGC Gly 390	TTT Phe	TGC Cys	ATC Ile	GAC Asp	CTG Leu	1443
CTC Leu 395	ATC Ile	AAG Lys	CTG Leu	GCA Ala	CGG Arg 400	ACC Thr	ATG Met	AAC Asn	TTC Phe 405	ACC Thr	TAC Tyr	GAG Glu	GTG Val	CAC His	CTG Leu 410	1491
GTG Val	GCA Ala	GAT Asp	GGC Gly	AAG Lys 415	TTC Phe	GGC Gly	ACA Thr	CAG Gln	GAG Glu 420	CGG Arg	GTG Val	AAC Asn	AAC Asn	AGC Ser	AAC Asn 425	1539
AAG Lys	AAG Lys	GAG Glu	TGG Trp 430	AAT Asn	GGG Gly	ATG Met	ATG Met	GGC Gly 435	GAG Glu	CTG Leu	CTC Leu	AGC Ser	GGG Gly 440	CAG Gln	GCA Ala	1587
GAC Asp	ATG Met	ATC Ile 445	GTG Val	GCG Ala	CCG Pro	CTA Leu	ACC Thr 450	ATA Ile	AAC Asn	AAC Asn	GAG Glu 455	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	1635
ATC Ile 460	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro	TTC Phe 465	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 470	CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val	1683
AAG Lys 475	AAG Lys	GAG Glu	ATT Ile	CCC Pro	CGG Arg 480	AGC Ser	ACG Thr	CTG Leu	GAC Asp	TCG Ser 485	TTC Phe	ATG Met	CAG Gln	CCG Pro	TTC Phe 490	1731
CAG Gln	AGC Ser	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val	CAC His	GTG Val	GTG Val	GCC Ala	1779

495								500					505					
GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	1827		
Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys			
			510					515					520					
GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	1875		
Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala			
			525					530					535					
ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	1923		
Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly			
			540				545					550						
GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	1971		
Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly			
			555			560				565					570			
TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	2019		
Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe			
				575				580							585			
CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	2067		
Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro			
			590					595						600				
CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	2115		
Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln			
			605				610						615					
AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGC	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	2163		
Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met			
			620				625					630						
TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	2211		
Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile			
					640					645					650			
CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	2259		
Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala			
				655					660					665				
GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	2307		
Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly			
			670					675						680				
GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	2355		
Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser			
			685				690					695						
CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	2403		
Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn			
			700				705					710						
GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	2451		
Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys			
					720					725					730			
GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	2499		
Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala			
				735					740					745				
GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	2547		
Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu			
				750				755					760					
ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	2595		

Ile Phe	Ile Glu	Ile Ala	Tyr Lys	Arg His	Lys Asp	Ala Arg	Arg Lys	
765			770			775		
CAG ATG	CAG CTG	GCC TTT	GCC GCC	GTT AAC	GTG TGG	CGG AAG	AAC CTG	2643
Gln Met	Gln Leu	Ala Phe	Ala Ala	Val Asn	Val Trp	Arg Lys	Asn Leu	
780			785					
CAG GAT	AGA AAG	AGT GGT	AGA GCA	GAG CCT	GAC CCT	AAA AAG	AAA GCC	2691
Gln Asp	Arg Lys	Ser Gly	Arg Ala	Glu Pro	Asp Pro	Lys Lys	Lys Ala	
795		800			805		810	
ACA TTT	AGG GCT	ATC ACC	TCC ACC	CTG GCT	TCC AGC	TTC AAG	AGG CGT	2739
Thr Phe	Arg Ala	Ile Thr	Ser Thr	Leu Ala	Ser Ser	Phe Lys	Arg Arg	
		815			820		825	
AGG TCC	TCC AAA	GAC ACG	AGC ACC	GGG GGT	GGA CGC	GGT GCT	TTG CAA	2787
Arg Ser	Ser Lys	Asp Thr	Ser Thr	Gly Gly	Gly Arg	Gly Ala	Leu Gln	
	830			835		840		
AAC CAA	AAA GAC	ACA GTG	CTG CCG	CGA CGC	GCT ATT	GAG AGG	GAG GAG	2835
Asn Gln	Lys Asp	Thr Val	Leu Pro	Arg Arg	Ala Ile	Glu Arg	Glu Glu	
	845		850			855		
GGC CAG	CTG CAG	CTG TGT	TCC CGT	CAT AGG	GAG AGC	TGAGACTCCC		2881
Gly Gln	Leu Gln	Leu Cys	Ser Arg	His Arg	Glu Ser			
860			865		870			
CGCCCGCCCT	CCTCTGCCCC	CTCCCCCGCA	GACAGACAGA	CAGACGGACG	GGACAGCGGC			2941
CCGGCCACG	CAGAGCCCCG	GAGCACCACG	GGGTCCGGGG	AGGAGCACCC	CCAGCCTCCC			3001
CCAGGCTGCG	CCTGCCCCGC	CGCCGGTTGG	CCGGCTGGCC	GGTCCACCCC	GTCCCGGCCC			3061
CGCGCGTGCC	CCCAGCGTGG	GGCTAACGGG	CGCCTTGTCT	GTGTATTTCT	ATTTTGCAGC			3121
AGTACCATCC	CACTGATATC	ACGGGCCCCG	TCAACCTCTC	AGATCCCTCG	GTCAGCACCG			3181
TGGTGTGAGG	CCCCCGGAGG	CGCCACCTG	CCCAGTTAGC	CCGGCCAAGG	AACTGATGG			3241
GTCCTGCTGC	TCGGGAAGGC	CTGAGGGAAG	CCCACCCGCC	CCAGAGACTG	CCCACCCTGG			3301
GCCTCCCGTC	CGTCCGCCCC	CCCACCCCGC	TGCCTGGCGG	GCAGCCCCTG	CTGGACCAAG			3361
GTGCGGACCG	GAGCGGCTGA	GGACGGGGCA	GAGCTGAGTC	GGCTGGGCAG	GGCCGCAGGG			3421
CGCTCCGGCA	GAGGCAGGCC	CCTGGGGTCT	CTGAGCAGTG	GGGAGCGGGG	GCTAACTGCC			3481
CCCAGGCGGA	GGGGCTTGGA	GCAGAGACGG	CAGCCCCATC	CTTCCCGCAG	CACCAGCCTG			3541
AGCCACAGTG	GGGCCCCATG	CCCAGCTGG	CTGGGTCGCC	CCTCCTCGGG	CGCCTGCGCT			3601
CCTCTGCAGC	CTGAGCTCCA	CCCTCCCCTC	TTCTTGCGGC	ACCGCCCACC	AAACACCCCG			3661
TCTGCCCTTT	GACGCCACAC	GCCGGGGCTG	GCGCTGCCCT	CCCCCACGGC	CGTCCCTGAC			3721
TTCCAGCTG	GCAGCGCCTC	CCGCCGCCTC	GGGCCGCCTC	CTCCAGAATC	GAGAGGGCTG			3781
AGCCCCCTCCT	CTCCTCGTCC	GGCCTGCAGC	ACAGAAGGGG	GCCTCCCCGG	GGGTCCCCGG			3841
ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	GGGCACGGGA	GAGCGCCACC			3901
CGCCCGCCCT	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCCG	CCACCTTGTA	CAGAACCAGC			3961
ACTCCAGGG	CCCAGCGCG	TGCCTTCCCC	GTGCGCAGCC	GCGCTCTGCC	CCTCCGTCCC			4021
CAGGGTGCAG	GCGCGCACCG	CCCAACCCCC	ACCTCCCGGT	GTATGCAGTG	GTGATGCCTA			4081

AAGGAATGTC ACG

4094

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 870 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	1	5	10	15
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	20	25	30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln	35	40	45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser	50	55	60	
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu	65	70	75	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro	85	90	95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	100	105	110	
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	115	120	125	
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	130	135	140	
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	145	150	155	
Asn	His	Ile	Ile	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	165	170	175		
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu	180	185	190	
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	195	200	205	
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	210	215	220	
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	225	230	235	
Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	245	250	255	
Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	260	265	270	
Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	275	280	285	



Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val
290						295					300				
Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys
305					310					315					320
Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His
				325					330					335	
Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys
			340					345					350		
Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys
		355					360					365			
Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro
	370					375					380				
Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg
385					390					395					400
Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe
				405					410					415	
Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly
			420					425					430		
Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro
		435					440					445			
Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro
	450					455					460				
Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg
465					470					475					480
Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu
				485					490					495	
Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu
			500					505					510		
Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu
		515					520					525			
Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly
	530					535					540				
Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser
545					550					555					560
Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val
				565					570					575	
Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro
				580				585					590		
Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser
		595					600					605			
Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr
	610					615					620				
Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys
625					630					635					640
His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn

645

650

655

Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala
			660					665					670		
Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser
		675					680					685			
Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val
	690					695					700				
Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu
	705				710					715					720
Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala
				725					730					735	
Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val
			740					745					750		
Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala
		755					760					765			
Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe
	770					775					780				
Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly
	785				790					795					800
Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr
			805						810					815	
Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr
		820						825					830		
Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val
		835				840						845			
Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu	Gly	Gln	Leu	Gln	Leu	Cys
	850					855					860				
Ser	Arg	His	Arg	Glu	Ser										
	865				870										

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..2826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCAGGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120

CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGCGCG	GGCGAGCGCA	180										
GGACGGCCCCG	GAAGCCCCCG	GGGGGATGCG	CCGAGGGCCC	CGCGTTCCCG	CCGCGCAGAG	240										
CCAGGCCCCGC	GGCGTGAGCC	C	ATG	AGC	ACC	ATG	CGC	CTG	CTG	ACG	CTC	GCC	291			
			Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	10			
			1				5									
CTG	CTG	TTC	TCC	TGC	TCC	GTC	GCC	CGT	GCC	GCG	TGC	GAC	CCC	AAG	ATC	339
Leu	Leu	Phe	Ser	Cys	Ser	Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	
			15						20					25		
GTC	AAC	ATT	GGC	GCG	GTG	CTG	AGC	ACG	CGG	AAG	CAC	GAG	CAG	ATG	TTC	387
Val	Asn	Ile	Gly	Ala	Val	Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	
			30					35					40			
CGC	GAG	GCC	GTG	AAC	CAG	GCC	AAC	AAG	CGG	CAC	GGC	TCC	TGG	AAG	ATT	435
Arg	Glu	Ala	Val	Asn	Gln	Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	
		45					50					55				
CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
	60					65					70					
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
	75				80					85					90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CGG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
	155				160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	JAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	
			190					195					200			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	JAG	CTG	GAG	GCC	CGG	GTC	915
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
		205					210					215				
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
		220				225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	
	235				240					245					250	

CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	1059
Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	
				255					260					265		
ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	1107
Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	
			270					275					280			
TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	1155
Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	
		285					290					295				
TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	1203
Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	
	300					305						310				
GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	1251
Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	
315					320					325					330	
AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	1299
Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	
				335					340					345		
CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	1347
Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	
			350					355					360			
GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	1395
Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	
		365					370					375				
CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	1443
Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	
	380					385					390					
CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	1491
Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	
	395				400					405					410	
GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	1539
Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	
				415					420					425		
AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	1587
Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	
			430					435					440			
GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	1635
Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	
		445					450					455				
ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	1683
Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	
	460					465					470					
AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	1731
Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	
	475				480					485					490	
CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	1779
Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	
			495					500						505		
GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	1827
Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	

			510				515				520							
GTG Val	AAC Asn	AGC Ser 525	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu 530	GAC Asp	GCA Ala	CTG Leu	ACC Thr	CTG Leu 535	TCC Ser	TCG Ser	GCC Ala		1875	
ATG Met	TGG Trp 540	TTC Phe	TCC Ser	TGG Trp	GGC Gly	GTC Val 545	CTG Leu	CTC Leu	AAC Asn	TCC Ser	GGC Gly 550	ATC Ile	GGG Gly	GAA Glu	GGC Gly		1923	
GCC Ala 555	CCC Pro	AGA Arg	AGC Ser	TTC Phe	TCA Ser 560	GCG Ala	CGC Arg	ATC Ile	CTG Leu	GGC Gly 565	ATG Met	GTG Val	TGG Trp	GCC Ala	GGC Gly 570		1971	
TTT Phe	GCC Ala	ATG Met	ATC Ile	ATC Ile 575	GTG Val	GCC Ala	TCC Ser	TAC Tyr	ACC Thr 580	GCC Ala	AAC Asn	CTG Leu	GCG Ala	GCC Ala 585	TTC Phe		2019	
CTG Leu	GTG Val	CTG Leu	GAC Asp 590	CGG Arg	CCG Pro	GAG Glu	GAG Glu	CGC Arg 595	ATC Ile	ACG Thr	GGC Gly	ATC Ile	AAC Asn 600	GAC Asp	CCT Pro		2067	
CGG Arg	CTG Leu	AGG Arg 605	AAC Asn	CCC Pro	TCG Ser	GAC Asp	AAG Lys 610	TTT Phe	ATC Ile	TAC Tyr	GCC Ala	ACG Thr 615	GTG Val	AAG Lys	CAG Gln		2115	
AGC Ser	TCC Ser 620	GTG Val	GAT Asp	ATC Ile	TAC Tyr	TTC Phe 625	CGG Arg	CGC Arg	CAG Gln	GTG Val	GAG Glu 630	CTG Leu	AGC Ser	ACC Thr	ATG Met		2163	
TAC Tyr 635	CGG Arg	CAT His	ATG Met	GAG Glu	AAG Lys 640	CAC His	AAC Asn	TAC Tyr	GAG Glu	AGT Ser 645	GCG Ala	GCG Ala	GAG Glu	GCC Ala	ATC Ile 650		2211	
CAG Gln	GCC Ala	GTG Val	AGA Arg	GAC Asp 655	AAC Asn	AAG Lys	CTG Leu	CAT His	GCC Ala 660	TTC Phe	ATC Ile	TGG Trp	GAC Asp	TCG Ser 665	GCG Ala		2259	
GTG Val	CTG Leu	GAG Glu	TTC Phe 670	GAG Glu	GCC Ala	TCG Ser	CAG Gln	AAG Lys 675	TGC Cys	GAC Asp	CTG Leu	GTG Val	ACG Thr 680	ACT Thr	GGA Gly		2307	
GAG Glu	CTG Leu	TTT Phe 685	TTC Phe	CGC Arg	TCG Ser	GGC Gly	TTC Phe 690	GGC Gly	ATA Ile	GGC Gly	ATG Met	CGC Arg 695	AAA Lys	GAC Asp	AGC Ser		2355	
CCC Pro	TGG Trp 700	AAG Lys	CAG Gln	AAC Asn	GTC Val	TCC Ser 705	CTG Leu	TCC Ser	ATC Ile	CTC Leu	AAG Lys 710	TCC Ser	CAC His	GAG Glu	AAT Asn		2403	
GGC Gly 715	TTC Phe	ATG Met	GAA Glu	GAC Asp	CTG Leu 720	GAC Asp	AAG Lys	ACG Thr	TGG Trp	GTT Val 725	CGG Arg	TAT Tyr	CAG Gln	GAA Glu	TGT Cys 730		2451	
GAC Asp	TCG Ser	CGC Arg	AGC Ser	AAC Asn 735	GCC Ala	CCT Pro	GCG Ala	ACC Thr	CTT Leu 740	ACT Thr	TTT Phe	GAG Glu	AAC Asn	ATG Met 745	GCC Ala		2499	
GGG Gly	GTC Val	TTC Phe	ATG Met 750	CTG Leu	GTA Val	GCT Ala	GGG Gly	GGC Gly 755	ATC Ile	GTG Val	GCC Ala	GGG Gly 760	ATC Ile	TTC Phe	CTG Leu		2547	
ATT Ile	TTC Phe	ATC Ile 765	GAG Glu	ATT Ile	GCC Ala	TAC Tyr	AAG Lys 770	CGG Arg	CAC His	AAG Lys	GAT Asp 775	GCT Ala	CGC Arg	CGG Arg	AAG Lys		2595	
CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG		2643	

Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu		
780						785					790						
CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	2691	
Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala		
795					800					805					810		
ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	TTC	AAG	AGG	CGT	2739	
Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg		
				815					820					825			
AGG	TCC	TCC	AAA	GAC	ACG	CAG	TAC	CAT	CCC	ACT	GAT	ATC	ACG	GGC	CCG	2787	
Arg	Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro		
			830					835					840				
CTC	AAC	CTC	TCA	GAT	CCC	TCG	GTC	AGC	ACC	GTG	GTG	TGAGGCCCCC				2833	
Leu	Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val						
	845						850					855					
GGAGGCGCCC	ACCTGCCCAG	TTAGCCCGGC	CAAGGACACT	GATGGGTCCT	GCTGCTCGGG											2893	
AAGGCCTGAG	GGAAGCCCAC	CCGCCCCAGA	GACTGCCCAC	CCTGGGCCTC	CCGTCCGTCC											2953	
GCCCCCCCAC	CCCCTGCCT	GGCGGGCAGC	CCCTGCTGGA	CCAAGGTGCG	GACCGGAGCG											3013	
GCTGAGGACG	GGGCAGAGCT	GAGTCGGCTG	GGCAGGGCCG	CAGGGCGCTC	CGGCAGAGGC											3073	
AGGCCCCCTGG	GGTCTCTGAG	CAGTGGGGAG	CGGGGGCTAA	CTGCCCCCAG	GCGGAGGGGC											3133	
TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	CGCAGCACCA	GCCTGAGCCA	CAGTGGGGCC											3193	
CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTC	TCGGGCGCCT	GCGCTCCTCT	GCAGCCTGAG											3253	
CTCCACCCTC	CCCTCTTCTT	GCGGCACCGC	CCACCAAACA	CCCCGTCTGC	CCCTTGACGC											3313	
CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	ACGGCCGTCC	CTGACTTCCC	AGCTGGCAGC											3373	
GCCTCCCGCC	GCCTCGGGCC	GCCTCCTCCA	GAATCGAGAG	GGCTGAGCCC	CTCCTCTCCT											3433	
CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	CCCGGGGGTC	CCCGGACGCT	GGCTCGGGAC											3493	
TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	CGGGAGAGCG	CCACCCGCCC	GCCCCCGCCC											3553	
TCGCTCCGGG	TGCGTGACCG	GCCCCGCCACC	TTGTACAGAA	CCAGCACTCC	CAGGGCCCCGA											3613	
GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	CTGCCCCCTCC	GTCCCCAGGG	TGCAGGCGCG											3673	
CACCGCCCCA	CCCCCACCTC	CCGGTGTATG	CAGTGGTGAT	GCCTAAAGGA	ATGTCACG											3731	

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 854 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser		
1				5					10					15			
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val		
	20							25					30				

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
 35 40 45  
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
 50 55 60  
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
 65 70 75 80  
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
 85 90 95  
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
 100 105 110  
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
 115 120 125  
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
 130 135 140  
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
 145 150 155 160  
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
 165 170 175  
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
 180 185 190  
 Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
 195 200 205  
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
 210 215 220  
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
 225 230 235 240  
 Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val  
 245 250 255  
 Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe  
 260 265 270  
 Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu  
 275 280 285  
 Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val  
 290 295 300  
 Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys  
 305 310 315 320  
 Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His  
 325 330 335  
 Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys  
 340 345 350  
 Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys  
 355 360 365  
 Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro  
 370 375 380  
 Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg

385		390		395		400
Thr Met Asn Phe	Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe					
	405			410		415
Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly						
	420		425			430
Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro						
	435		440			445
Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro						
	450		455			460
Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg						
	465		470		475	480
Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu						
	485		490			495
Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu						
	500		505			510
Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu						
	515		520			525
Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly						
	530		535			540
Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser						
	545		550		555	560
Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val						
	565		570			575
Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro						
	580		585			590
Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser						
	595		600			605
Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr						
	610		615			620
Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys						
	625		630		635	640
His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn						
	645		650			655
Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala						
	660		665			670
Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser						
	675		680			685
Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val						
	690		695			700
Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu						
	705		710		715	720
Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala						
	725		730			735
Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val						



740	745	750
Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala		
755	760	765
Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe		
770	775	780
Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly		
785	790	795
Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr		
805	810	815
Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr		
820	825	830
Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro		
835	840	845
Ser Val Ser Thr Val Val		
850		

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3007 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 262..2988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	

CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
60						65					70					
GCT	CTC	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
75					80					85					90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
140						145					150					
ATG	CGT	GTG	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Val	Ser	Asp	Asp		
155					160					165				170		
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	
			190					195					200			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
		205					210					215				
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
		220				225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	
235					240					245					250	
CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	1059
Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	
				255					260					265		
ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	1107
Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	
			270					275					280			
TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	1155
Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	
		285					290					295				
TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	1203
Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	
		300				305					310					
GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	1251
Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	
315					320					325					330	

AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	1299
Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	
				335					340					345		
CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	1347
Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	
			350					355					360			
GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	1395
Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	
		365					370					375				
CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	1443
Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	
	380					385					390					
CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	1491
Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	
	395				400					405					410	
GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	1539
Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	
				415					420					425		
AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	1587
Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	
			430					435					440			
GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	1635
Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	
		445					450					455				
ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	1683
Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	
	460					465					470					
AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	1731
Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	
	475				480					485					490	
CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	1779
Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	
			495					500					505			
GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	1827
Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	
		510					515					520				
GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	1875
Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	
		525					530					535				
ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	1923
Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	
	540				545						550					
GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	1971
Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	
	555				560					565					570	
TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	2019
Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	
			575					580					585			
CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	2067
Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	
			590					595					600			

CGG Arg	CTG Leu	AGG Arg 605	AAC Asn	CCC Pro	TCG Ser	GAC Asp	AAG Lys 610	TTT Phe	ATC Ile	TAC Tyr	GCC Ala	ACG Thr 615	GTG Val	AAG Lys	CAG Gln	211
AGC Ser	TCC Ser 620	GTG Val	GAT Asp	ATC Ile	TAC Tyr	TTC Phe 625	CGG Arg	CGC Arg	CAG Gln	GTG Val	GAG Glu 630	CTG Leu	AGC Ser	ACC Thr	ATG Met	2160
TAC Tyr 635	CGG Arg	CAT His	ATG Met	GAG Glu	AAG Lys 640	CAC His	AAC Asn	TAC Tyr	GAG Glu	AGT Ser 645	GCG Ala	GCG Ala	GAG Glu	GCC Ala	ATC Ile 650	2211
CAG Gln	GCC Ala	GTG Val	AGA Arg	GAC Asp 655	AAC Asn	AAG Lys	CTG Leu	CAT His	GCC Ala 660	TTC Phe	ATC Ile	TGG Trp	GAC Asp	TCG Ser 665	GCG Ala	2259
GTG Val	CTG Leu	GAG Glu 670	TTC Phe	GAG Glu	GCC Ala	TCG Ser	CAG Gln	AAG Lys 675	TGC Cys	GAC Asp	CTG Leu	GTG Val	ACG Thr 680	ACT Thr	GGA Gly	2307
GAG Glu	CTG Leu	TTT Phe 685	TTC Phe	CGC Arg	TCG Ser	GGC Gly	TTC Phe 690	GGC Gly	ATA Ile	GGC Gly	ATG Met	CGC Arg 695	AAA Lys	GAC Asp	AGC Ser	2355
CCC Pro	TGG Trp 700	AAG Lys	CAG Gln	AAC Asn	GTC Val	TCC Ser 705	CTG Leu	TCC Ser	ATC Ile	CTC Leu	AAG Lys 710	TCC Ser	CAC His	GAG Glu	AAT Asn	2403
GGC Gly 715	TTC Phe	ATG Met	GAA Glu	GAC Asp	CTG Leu 720	GAC Asp	AAG Lys	ACG Thr	TGG Trp	GTT Val 725	CGG Arg	TAT Tyr	CAG Gln	GAA Glu	TGT Cys 730	2451
GAC Asp	TCG Ser	CGC Arg	AGC Ser	AAC Asn 735	GCC Ala	CCT Pro	GCG Ala	ACC Thr	CTT Leu 740	ACT Thr	TTT Phe	GAG Glu	AAC Asn	ATG Met 745	GCC Ala	2499
GGG Gly	GTC Val	TTC Phe 750	ATG Met	CTG Leu	GTA Val	GCT Ala	GGG Gly	GGC Gly 755	ATC Ile	GTG Val	GCC Ala	GGG Gly 760	ATC Ile	TTC Phe	CTG Leu	2547
ATT Ile	TTC Phe 765	ATC Ile	GAG Glu	ATT Ile	GCC Ala	TAC Tyr	AAG Lys 770	CGG Arg	CAC His	AAG Lys	GAT Asp	GCT Ala 775	CGC Arg	CGG Arg	AAG Lys	2595
CAG Gln 780	ATG Met	CAG Gln	CTG Leu	GCC Ala	TTT Phe	GCC Ala 785	GCC Ala	GTT Val	AAC Asn	GTG Val	TGG Trp 790	CGG Arg	AAG Lys	AAC Asn	CTG Leu	2643
CAG Gln 795	GAT Asp	AGA Arg	AAG Lys	AGT Ser	GGT Gly 800	AGA Arg	GCA Ala	GAG Glu	CCT Pro	GAC Asp 805	CCT Pro	AAA Lys	AAG Lys	AAA Lys	GCC Ala 810	2691
ACA Thr	TTT Phe	AGG Arg	GCT Ala	ATC Ile 815	ACC Thr	TCC Ser	ACC Thr	CTG Leu	GCT Ala 820	TCC Ser	AGC Ser	TTC Phe	AAG Lys	AGG Arg 825	CGT Arg	2739
AGG Arg	TCC Ser	TCC Ser	AAA Lys 830	GAC Asp	ACG Thr	CTG Leu	GCT Ala	CGG Arg 835	GAC Asp	TGT Cys	CTT Leu	CAA Gln	CCC Pro 840	TGC Cys	CCT Pro	2787
GCA Ala	CCT Pro	TGG Trp 845	GCA Ala	CGG Arg	GAG Glu	AGC Ser	GCC Ala 850	ACC Thr	CGC Arg	CCG Pro	CCC Pro	CCG Pro 855	CCC Pro	TCG Ser	CTC Leu	2805
CGG Arg	GTG Val 860	CGT Arg	GAC Asp	CGG Arg	CCC Pro	GCC Ala 865	ACC Thr	TTG Leu	TAC Tyr	AGA Arg 870	ACC Thr	AGC Ser	ACT Thr	CCC Pro	AGG Arg	2883

GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT	2931
Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg	
875 880 885 890	
CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG	2979
Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met	
895 900 905	
CAG TGG TGATGCCTAA AGGAATGTCA CG	3007
Gln Trp	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
	20							25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
	35						40					45			
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50					55					60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65				70			75						80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
			85				90						95		
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
		100					105						110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
	115						120					125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
	130					135					140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
	145				150				155					160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
			165					170						175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu
			180					185					190		
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu
	195						200					205			
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser
	210					215					220				
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met

225		230		235		240
Thr Gly Asn Thr	Asn Ile Trp Lys Thr Gly	Pro Leu Phe Lys Arg Val				
	245	250			255	
Leu Met Ser Ser	Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe					
	260	265			270	
Asn Glu Asp Gly	Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu					
	275	280			285	
Gln Asn Arg Lys	Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val					
	290	295			300	
Ile Pro Asn Asp	Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys					
	305	310			315	320
Pro Arg Gly Tyr	Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His					
	325	330			335	
Gln Glu Pro Phe	Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys					
	340	345			350	
Lys Glu Glu Phe	Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys					
	355	360			365	
Thr Gly Pro Asn	Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro					
	370	375			380	
Gln Cys Cys Tyr	Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg					
	385	390			395	400
Thr Met Asn Phe	Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe					
	405	410			415	
Gly Thr Gln Glu	Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly					
	420	425			430	
Met Met Gly Glu	Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro					
	435	440			445	
Leu Thr Ile Asn	Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro					
	450	455			460	
Phe Lys Tyr Gln	Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg					
	465	470			475	480
Ser Thr Leu Asp	Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu					
	485	490			495	
Leu Val Gly Leu	Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu					
	500	505			510	
Asp Arg Phe Ser	Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu					
	515	520			525	
Glu Glu Asp Ala	Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly					
	530	535			540	
Val Leu Leu Asn	Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser					
	545	550			555	560
Ala Arg Ile Leu	Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val					
	565	570			575	
Ala Ser Tyr Thr	Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro					
	580	585			590	

Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	595	600	605
Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	610	615	620
Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	625	630	635
His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	645	650	655
Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	660	665	670
Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	675	680	685
Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	690	695	700
Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	705	710	715
Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	725	730	735
Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	740	745	750
Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	755	760	765
Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	770	775	780
Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	785	790	795
Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	805	810	815
Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr	820	825	830
Leu	Ala	Arg	Asp	Cys	Leu	Gln	Pro	Cys	Pro	Ala	Pro	Trp	Ala	Arg	Glu	835	840	845
Ser	Ala	Thr	Arg	Pro	Pro	Pro	Pro	Ser	Leu	Arg	Val	Arg	Asp	Arg	Pro	850	855	860
Ala	Thr	Leu	Tyr	Arg	Thr	Ser	Thr	Pro	Arg	Ala	Arg	Ala	Arg	Ala	Phe	865	870	875
Pro	Val	Arg	Ser	Arg	Ala	Leu	Pro	Leu	Arg	Pro	Gln	Gly	Ala	Gly	Ala	885	890	895
His	Arg	Pro	Thr	Pro	Thr	Ser	Arg	Cys	Met	Gln	Trp					900	905	

(2) INFORMATION FOR SEQ ID NO:35:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3998 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCSCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg 5 Leu Leu Thr Leu Ala 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	



175																180				185				
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867								
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu									
			190					195					200											
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915								
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe									
		205					210					215												
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963								
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu									
	220					225					230													
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011								
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala									
235					240					245					250									
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059								
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr									
				255					260					265										
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107								
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr									
			270					275					280											
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155								
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu									
		285					290					295												
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203								
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His									
	300					305					310													
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CCG	GGC	TGC	GTG	1251								
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val									
315					320					325					330									
GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	1299								
Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu									
				335					340					345										
ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	1347								
Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn									
			350					355					360											
GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	1395								
Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln									
		365					370					375												
AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	1443								
Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile									
	380					385					390													
CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	1491								
Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro									
395					400					405					410									
CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	1539								
Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln									
				415					420					425										
GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	1587								
Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys									
			430					435					440											
GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	1633								

Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	
		445					450					455				
GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	1683
Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	
		460					465				470					
TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	1731
Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	
		475				480				485					490	
ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	1779
Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	
				495					500					505		
ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	1827
Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	
			510					515					520			
ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	1875
Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	
		525					530					535				
ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	1923
Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	
		540				545					550					
AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	1971
Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	
		555				560				565					570	
ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	2019
Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	
				575					580					585		
GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	2067
Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	
			590					595					600			
CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	
		605					610					615				
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	
		620				625					630					
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
				635		640				645					650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660					665		
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
			670					675					680			
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
			685				690					695				
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
		700				705					710					

CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GGC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883
GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln 910 915 920	3027
TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser 925 930 935	3075
GTC AGC ACC GTG GTG TGAGGCCCCC GGAGGCGCCC ACCTGCCCAG TTAGCCCCGGC Val Ser Thr Val Val 940	3130
CAAGGACACT GATGGGTCTT GCTGCTCGGG AAGGCCTGAG GGAAGCCCCAC CCGCCCCAGA	3190
GACTGCCCCAC CCTGGGCCTC CCGTCCGTTC GCCCGCCCCAC CCCGCTGCCT GGCGGGCAGC	3250
CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GTTGAGGACG GGGCAGAGCT GAGTCGGCTG	3310
GGCAGGGCCG CAGGGCGCTC CGGCAGAGGC AGGCCCTGG GGTCTCTGAG CAGTGGGAG	3370

CGGGGGCTAA CTGCCCCCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC	3430
CGCAGCACCA GCCTGAGCCA CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCGCCCCCTCC	3490
TCGGGGCGCCT GCGCTCCTCT GCAGCCTGAG CTCACCCCTC CCCTCTTCTT GCGGCACCGC	3550
CCACCAAACA CCCCCTCTGC CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC	3610
ACGGCCGTCC CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA	3670
GAATCGAGAG GGCTGAGCCC CTCCTCTCCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC	3730
CCCGGGGGTC CCCGGACGCT GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA	3790
CGGGAGAGCG CCACCCGCCC GCCCCCGCCC TCGCTCCGGG TCGGTGACCG GCCCCCACC	3850
TTGTACAGAA CCAGCACTCC CAGGGCCCGA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT	3910
CTGCCCCCTCC GTCCCCAGGG TGCAGGCGCG CACCGCCCAA CCCCCACCTC CCGGTGTATG	3970
CAGTGGTGAT GCCTAAAGGA ATGTCACG	3998

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 943 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
	20							25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
	35					40					45				
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50				55					60					
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65				70			75						80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
			85					90						95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
		100					105					110			
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
	115					120					125				
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
	130				135					140					
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
145				150				155						160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
			165					170						175	

Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys		
			180					185					190				
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg		
		195					200					205					
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn		
	210					215					220						
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile		
225					230					235					240		
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala		
				245				250						255			
Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu		
			260					265					270				
Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu		
		275					280					285					
Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp		
	290					295					300						
Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu		
305					310					315					320		
Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp		
				325					330					335			
Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala		
			340					345					350				
Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys		
		355					360					365					
Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln		
	370					375					380						
Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile		
385					390					395					400		
Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser		
				405					410					415			
Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val		
			420					425					430				
Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn		
		435					440					445					
Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser		
	450					455					460						
Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys		
465					470					475					480		
Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu		
				485					490					495			
Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn		
			500					505					510				
Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser		
		515					520					525					
Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg		

530	535	540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr 545 550 555 560		
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met 565 570 575		
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His 580 585 590		
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly 595 600 605		
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu 610 615 620		
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile 625 630 635 640		
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val 645 650 655		
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu 660 665 670		
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile 675 680 685		
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr 690 695 700		
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu 705 710 715 720		
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala 725 730 735		
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp 740 745 750		
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val 755 760 765		
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg 770 775 780		
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser 785 790 795 800		
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr 805 810 815		
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu 820 825 830		
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly 835 840 845		
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala 850 855 860		
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg 865 870 875 880		
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys		

(2) INFORMATION FOR SEO ID NO:37:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAAGCCGGGC	GTTCGGAGCT	GTGCCC GGCC	CCGCTTCAGC	ACC CGCGACA	GCGCCGGCCG		60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC		120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGCCG	GGCGAGCGCA		180
GGACGGCCCCG	GAAGCCCCCG	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG		240
CCAGGCCCCGC	GGCCCCGAGCC	C ATG AGC ACC ATG CGC	CTG CTG ACG CTC GCC				291
		Met Ser Thr Met Arg	Leu Leu Thr Leu Ala				
		1	5			10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC							339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile							
		15				20	25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC							387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe							
		30				35	40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT							435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile							
		45				50	55
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG							483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met							
		60				65	70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC							531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile							
		75				80	85
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT							579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro							
				95		100	105

GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
	155				160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
	235				240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
				255				260						265		
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
			270					275					280			
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
		285					290					295				
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
	300					305					310					
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
	315				320				325						330	
GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	1299
Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	
				335				340						345		
ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	1347
Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	
			350					355					360			
GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	1395
Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	





Leu 635	Leu	Asn	Ser	Gly 640	Ile	Gly	Glu	Gly	Ala	Pro 645	Arg	Ser	Phe	Ser	Ala 650	
CGC Arg	ATC Ile	CTG Leu	GGC Gly	ATG Met 655	GTG Val	TGG Trp	GCC Ala	GGC Gly	TTT Phe 660	GCC Ala	ATG Met	ATC Ile	ATC Ile	GTG Val 665	GCC Ala	2259
TCC Ser	TAC Tyr	ACC Thr	GCC Ala 670	AAC Asn	CTG Leu	GCG Ala	GCC Ala	TTC Phe 675	CTG Leu	GTG Val	CTG Leu	GAC Asp 680	CGG Arg	CCG Pro	GAG Glu	2307
GAG Glu	CGC Arg	ATC Ile 685	ACG Thr	GGC Gly	ATC Ile	AAC Asn	GAC Asp 690	CCT Pro	CGG Arg	CTG Leu	AGG Arg	AAC Asn 695	CCC Pro	TCG Ser	GAC Asp	2355
AAG Lys 700	TTT Phe	ATC Ile	TAC Tyr	GCC Ala	ACG Thr	GTG Val 705	AAG Lys	CAG Gln	AGC Ser	TCC Ser	GTG Val 710	GAT Asp	ATC Ile	TAC Tyr	TTC Phe	2403
CGG Arg 715	CGC Arg	CAG Gln	GTG Val	GAG Glu 720	CTG Leu	AGC Ser	ACC Thr	ATG Met	TAC Tyr	CGG Arg 725	CAT His	ATG Met	GAG Glu	AAG Lys	CAC His 730	2451
AAC Asn	TAC Tyr	GAG Glu	AGT Ser	GCG Ala 735	GCG Ala	GAG Glu	GCC Ala	ATC Ile	CAG Gln 740	GCC Ala	GTG Val	AGA Arg	GAC Asp	AAC Asn 745	AAG Lys	2499
CTG Leu	CAT His	GCC Ala 750	TTC Phe	ATC Ile	TGG Trp	GAC Asp	TCG Ser	GCG Ala 755	GTG Val	CTG Leu	GAG Glu	TTC Phe	GAG Glu 760	GCC Ala	TCG Ser	2547
CAG Gln	AAG Lys	TGC Cys 765	GAC Asp	CTG Leu	GTG Val	ACG Thr	ACT Thr 770	GGA Gly	GAG Glu	CTG Leu	TTT Phe 775	TTC Phe	CGC Arg	TCG Ser	GGC Gly	2595
TTC Phe 780	GGC Gly	ATA Ile	GGC Gly	ATG Met	CGC Arg	AAA Lys 785	GAC Asp	AGC Ser	CCC Pro	TGG Trp	AAG Lys 790	CAG Gln	AAC Asn	GTC Val	TCC Ser	2643
CTG Leu 795	TCC Ser	ATC Ile	CTC Leu	AAG Lys	TCC Ser 800	CAC His	GAG Glu	AAT Asn	GGC Gly	TTC Phe 805	ATG Met	GAA Glu	GAC Asp	CTG Leu 810	GAC Asp	2691
AAG Lys	ACG Thr	TGG Trp	GTT Val	CGG Arg 815	TAT Tyr	CAG Gln	GAA Glu	TGT Cys	GAC Asp 820	TCG Ser	CGC Arg	AGC Ser	AAC Asn	GCC Ala 825	CCT Pro	2739
GCG Ala	ACC Thr	CTT Leu	ACT Thr 830	TTT Phe	GAG Glu	AAC Asn	ATG Met	GCC Ala 835	GGG Gly	GTC Val	TTC Phe	ATG Met	CTG Leu 840	GTA Val	GCT Ala	2787
GGG Gly	GGC Gly	ATC Ile 845	GTG Val	GCC Ala	GGG Gly	ATC Ile	TTC Phe	CTG Leu	ATT Ile	TTC Phe	ATC Ile	GAG Glu 855	ATT Ile	GCC Ala	TAC Tyr	2835
AAG Lys 860	CGG Arg	CAC His	AAG Lys	GAT Asp	GCT Ala	CGC Arg	CGG Arg	AAG Lys	CAG Gln	ATG Met	CAG Gln 870	CTG Leu	GCC Ala	TTT Phe	GCC Ala	2883
GCC Ala 875	GTT Val	AAC Asn	GTG Val	TGG Trp	CGG Arg 880	AAG Lys	AAC Asn	CTG Leu	CAG Gln	GAT Asp 885	AGA Arg	AAG Lys	AGT Ser	GGT Gly	AGA Arg 890	2931
GCA Ala	GAG Glu	CCT Pro	GAC Asp	CCT Pro 895	AAA Lys	AAG Lys	AAA Lys	GCC Ala	ACA Thr 900	TTT Phe	AGG Arg	GCT Ala	ATC Ile	ACC Thr	TCC Ser	2979

ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG	3027
Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu	
910 915 920	
GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC	3075
Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser	
925 930 935	
GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC	3123
Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala	
940 945 950	
ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC	3171
Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro	
955 960 965 970	
GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC	3219
Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His	
975 980 985	
CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA	3272
Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	
990 995	
CG	3274

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	

Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala		
				165					170					175			
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys		
			180					185					190				
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg		
		195					200					205					
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn		
	210					215					220						
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile		
	225				230					235					240		
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala		
			245					250						255			
Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu		
		260						265					270				
Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu		
		275					280					285					
Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp		
	290					295					300						
Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu		
	305				310					315					320		
Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp		
			325						330					335			
Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala		
		340						345					350				
Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys		
		355				360					365						
Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln		
	370					375					380						
Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile		
	385				390					395					400		
Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser		
			405						410					415			
Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val		
		420						425					430				
Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn		
		435					440					445					
Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser		
	450					455					460						
Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys		
	465				470					475					480		
Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu		
			485						490					495			
Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn		
		500						505					510				
Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser		

515	520	525
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg 530 535 540		
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr 545 550 555 560		
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met 565 570 575		
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His 580 585 590		
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly 595 600 605		
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu 610 615 620		
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile 625 630 635 640		
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val 645 650 655		
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu 660 665 670		
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile 675 680 685		
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr 690 695 700		
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu 705 710 715 720		
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala 725 730 735		
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp 740 745 750		
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val 755 760 765		
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg 770 775 780		
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser 785 790 795 800		
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr 805 810 815		
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu 820 825 830		
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly 835 840 845		
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala 850 855 860		
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		

865	870	875	880
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys	885	890	895
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe	900	905	910
Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln	915	920	925
Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro	930	935	940
Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser	945	950	955
Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu	965	970	975
Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser	980	985	990
Arg Cys Met Gln Trp	995		

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3070 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435

Arg	Glu	Ala	Val	Asn	Gln	Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	
		45					50					55				
CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
	60					65					70					
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
	75				80					85					90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
		140				145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
	155				160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
			175						180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
		220				225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
	235				240					245					250	
ACT	GTA	TAC	CGG	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
			270					275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
		300				305					310					

GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTG	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
315					320					325					330	
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
				335					340					345		
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
			350					355					360			
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
	365						370					375				
GTG	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
	380					385					390					
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
395					400					405					410	
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415					420					425		
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
			430					435					440			
GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	1635
Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	
			445				450					455				
CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	1683
Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	
			460			465					470					
GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	1731
Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	
475					480					485					490	
CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	1779
Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	
				495					500					505		
TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	1827
Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	
			510					515					520			
GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	1875
Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	
			525				530					535				
TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	1923
Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	
			540			545					550					
ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTG	CTG	CTC	AAC	TCC	1971
Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	
				560						565					570	
GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	2019
Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	
				575					580					585		



ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	2067
Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	
			590					595					600			
AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	2115
Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	
		605					610					615				
GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCC	GAC	AAG	TTT	ATC	TAC	2163
Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	
	620					625					630					
GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	2211
Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	
	635					640				645					650	
GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	2259
Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	
				655					660					665		
GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	2307
Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	
			670					675					680			
ATC	TGG	GAC	TCC	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCC	CAG	AAG	TGC	GAC	2355
Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	
		685					690					695				
CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCC	GGC	TTC	GGC	ATA	GGC	2403
Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	
	700					705					710					
ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	2451
Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	
	715				720					725					730	
AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	2499
Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	
				735					740					745		
CGG	TAT	CAG	GAA	TGT	GAC	TCC	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	2547
Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	
			750					755					760			
TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	2595
Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	
		765					770					775				
GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	2643
Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	
	780					785					790					
GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	2691
Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	
	795				800					805					810	
TGG	CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	2739
Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	
				815					820					825		
CCT	AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	2787
Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	
			830					835					840			
AGC	TTC	AAG	AGG	CGT	AGG	TCC	TCC	AAA	GAC	ACG	CTG	GCT	CGG	GAC	TGT	2835
Ser	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr	Leu	Ala	Arg	Asp	Cys	
		845					850					855				

CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG	2883
Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro	
860 865 870	
CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA	2931
Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg	
875 880 885 890	
ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC	2979
Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg	
895 900 905	
GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC	3027
Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro	
910 915 920	
ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG	3070
Thr Ser Arg Cys Met Gln Trp	
925 930	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 929 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys	
180 185 190	

Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg
		195					200					205			
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn
		210				215					220				
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile
225					230					235					240
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala
				245					250					255	
Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro
			260					265					270		
Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr
		275					280					285			
Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr
	290					295					300				
Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr
305					310					315					320
Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly
			325						330					335	
Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys
			340					345					350		
Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu
		355					360					365			
Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val
	370					375					380				
Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro
385					390					395					400
Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu
				405					410					415	
Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val
			420					425					430		
Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys
		435					440					445			
Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp
	450					455					460				
Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile
465					470					475					480
Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys
				485					490					495	
Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln
			500					505					510		
Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val
		515					520					525			
Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val
	530					535					540				
Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met

545		550		555		560
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala	565		570		575	
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe	580		585		590	
Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu	595		600		605	
Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg	610		615		620	
Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser	625		630		635	640
Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr	645		650		655	
Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln	660		665		670	
Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val	675		680		685	
Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu	690		695		700	
Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro	705		710		715	720
Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly	725		730		735	
Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp	740		745		750	
Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly	755		760		765	
Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile	770		775		780	
Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln	785		790		795	800
Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln	805		810		815	
Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr	820		825		830	
Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg	835		840		845	
Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala	850		855		860	
Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg	865		870		875	880
Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala	885		890		895	
Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro						

900	905	910
Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln		
915	920	925

Trp

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..2324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CC GGC CAC GTG TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT	47
Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp	
1 5 10 15	
GCG CCC CCC GCC ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG	95
Ala Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu	
20 25 30	
AGC TGG CGC CTC AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT	143
Ser Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile	
35 40 45	
CTG GCC CTG GGC GCC CAC AGC TAC TGG CGC CAG CAT GGA ACC CTG CCA	191
Leu Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro	
50 55 60	
GCC CCG CCC GGG GAC TGC CST GTT CAC CCT GGG CCC GTC AGC CCT GCC	239
Ala Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala	
65 70 75	
CGG GAG GCC TTC TAC AGG CAC CTA CTG AAT GTC ACC TGG GAG GGC CGA	287
Arg Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg	
80 85 90 95	
GAC TTC TCC TTC AGC CCT GGT GGG TAC CTG GTC CAG CCC ACC ATG GTG	335
Asp Phe Ser Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val	
100 105 110	
GTG ATC GCC CTC AAC CCG CAC CGC CTC TGG GAG ATG GTG GGG CGC TGG	383
Val Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp	
115 120 125	
GAG CAT GGC GTC CTA TAC ATG AAG TAC CCC GTG TGG CCT CGC TAC AGT	431
Glu His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser	
130 135 140	
GCC TCT CTG CAG CCT GTG GTG GAC AGT CGG CAC CTG ACG GTG GCC ACG	479
Ala Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr	
145 150 155	

CTG	GAA	GAG	CGG	CCC	TTT	GTC	ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	527
Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	
160					165					170					175	
GGA	GGC	TGT	GTC	CCC	AAC	ACC	GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	575
Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	
				180					185					190		
ACC	TTC	AGC	AGC	GGG	GAC	GTG	GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	623
Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	
			195					200					205			
GGA	TTC	TGC	ATC	GAC	ATC	CTC	AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	671
Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	
		210					215					220				
TCC	TAC	GAC	CTG	TAC	CTG	GTG	ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	719
Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	
	225					230					235					
CGC	GGC	GTA	TGG	AAC	GGC	ATG	ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	767
Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	
240					245					250					255	
GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	815
Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	
				260					265					270		
GTA	GAC	TTC	TCT	GTA	CCC	TTT	GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	863
Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	
			275					280					285			
GCT	CGC	AGC	AAT	GGC	ACC	GTC	TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	911
Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	
		290					295					300				
AGC	CCT	GCA	GTG	TGG	GTG	ATG	ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	959
Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	
	305					310					315					
GCC	ATC	ACC	GTC	TTC	ATG	TTC	GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	1007
Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	
320					325					330					335	
CAG	AAC	CTC	ACC	AGA	GGC	AAG	AAG	TCC	GGG	GGC	CCA	GCT	TTC	ACT	ATC	1055
Gln	Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	
				340					345					350		
GGC	AAG	TCC	GTG	TGG	CTG	CTG	TGG	GGG	CTG	GTC	TTC	AAC	AAC	TCA	GTG	1103
Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	
			355					360					365			
CCC	ATC	GAG	AAC	CCG	CGG	GGC	ACC	ACC	AGC	AAG	ATC	ATG	GTT	CTG	GTC	1151
Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	
		370					375					380				
TGG	GGC	TTC	TTT	GCT	GTC	ATC	TTC	CTC	GCC	AGA	TAC	ACG	GCC	AAC	CTG	1199
Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	
	385					390					395					
GCC	GCC	TTC	ATG	ATC	CAA	GAG	CAA	TAC	ATC	GAC	ACT	GTG	TCG	GGC	CTC	1247
Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	
400					405					410					415	
AGT	GAC	AAG	AAG	TTT	CAG	CGG	CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	1295
Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	

420								425								430	
TTC	GGC	ACG	GTG	CCC	AAC	GGC	AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	1343	
Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn		
435								440								445	
TAC	CCT	GAC	ATG	CAC	ACC	CAC	ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	1391	
Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val		
450								455								460	
GAG	GAC	GGC	CTC	ACC	AGC	CTC	AAG	ATG	GGC	AAG	GAC	GAG	GGC	TGC	AAG	1439	
Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Asp	Glu	Gly	Cys	Lys		
465								470								475	
CTG	GTC	ACC	ATT	GGG	TCT	GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	TAC	GGC	1487	
Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly		
480								485								490	
ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	CTG	GCG	1535	
Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala		
500								505								510	
CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GTG	1583	
Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val		
515								520								525	
TGG	CTC	TCA	GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	1631	
Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser		
530								535								540	
AAG	CTG	GAC	ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	ATG	CTG	CTG	GTG	1679	
Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val		
545								550								555	
GCC	ATG	GGG	CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	GAG	CAC	CTG	GTC	TAC	1727	
Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr		
560								565								570	
TGG	AAG	CTG	CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	TTC	CTG	1775	
Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu		
580								585								590	
CTG	GCT	TTC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	1823	
Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser		
595								600								605	
CTC	GCC	AGC	CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TCG	1871	
Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser		
610								615								620	
GCC	CAG	GCC	AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	1919	
Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val		
625								630								635	
ACC	ACG	GGC	GGC	GTA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	1967	
Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile		
640								645								650	
GAG	AAT	TGG	GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CCG	2015	
Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro		
660								665								670	
ACC	CCG	CGG	TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	2063	
Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro		
675								680								685	
CCA	GAG	CCG	AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	2111	

Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala		
	690						695					700					
GGG	ATT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	2159	
Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro		
	705					710					715						
GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	2207	
Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp		
	720				725					730					735		
GAG	GGG	CGG	TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	2255	
Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser		
				740					745					750			
GGC	TCC	GAG	CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	2303	
Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe		
			755					760					765				
CCT	CGA	GCC	GAC	CGA	TCC	GGC	CG									2326	
Pro	Arg	Ala	Asp	Arg	Ser	Gly											
			770														

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly	His	Val	Trp	Leu	Val	Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala		
1				5					10					15			
Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser		
		20					25				30						
Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu		
		35				40					45						
Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala		
	50				55					60							
Pro	Ala	Gly	Asp	Cys	Arg	Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg		
	65			70					75					80			
Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp		
			85					90						95			
Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val		
			100					105						110			
Ile	Ala	Leu	Asn	Arg	His	Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu		
	115						120					125					
His	Gly	Val	Leu	Tyr	Met	Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala		
	130					135					140						
Ser	Leu	Gln	Pro	Val	Val	Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu		
	145				150					155					160		
Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly		
			165						170					175			



Gly	Cys	Val	Pro	Asn	Thr	Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr
			180					185					190		
Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly
		195					200					205			
Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser
	210					215					220				
Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg
225					230					235					240
Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp
				245					250					255	
Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val
			260					265					270		
Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala
		275					280					285			
Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser
	290					295					300				
Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala
305					310					315					320
Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln
				325					330					335	
Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly
			340					345					350		
Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro
		355					360					365			
Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp
	370					375					380				
Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala
385					390					395					400
Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser
				405					410					415	
Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe
			420					425					430		
Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr
		435					440					445			
Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu
	450					455					460				
Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu
465					470					475					480
Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile
				485					490					495	
Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu
			500					505					510		
Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp
		515					520					525			

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Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys
530          535          540

Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala
545          550          555          560

Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp
          565          570          575

Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu
          580          585          590

Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu
595          600          605

Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala
610          615          620

Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr
625          630          635

Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu
          645          650          655

Asn Trp Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr
          660          665          670

Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro
675          680          685

Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala
690          695          700

Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly
705          710          715          720

Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu
          725          730          735

Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala
          740          745          750

Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro
755          760          765

Arg Ala Asp Arg Ser Gly
770

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 3...3698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TS	GAG	ATC	CAG	CCG	CTC	ACA	GTT	GGG	GTC	AAC	ACC	ACC	AAC	CCC	AGC	47
	Glu	Ile	Gln	Pro	Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	
	1				5				10						15	
AGC	CTC	CTC	ACC	CAG	ATC	TGC	GGC	CTC	CTG	GGT	GCT	GCC	CAC	GTC	CAC	95
Ser	Leu	Leu	Thr	Gln	Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	
				20				25						30		
GGC	ATT	GTC	TTT	GAG	GAC	AAC	GTG	GAC	ACC	GAG	GCG	GTG	GCC	CAG	ATC	143
Gly	Ile	Val	Phe	Glu	Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	
		35					40					45				
CTT	GAC	TTC	ATC	TCC	TCC	CAG	ACC	CAT	GTG	CCC	ATC	CTC	AGC	ATC	AGC	191
Leu	Asp	Phe	Ile	Ser	Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	
	50					55					60					
GGG	GGC	TCT	GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	239
Gly	Gly	Ser	Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	
	65					70				75						
CTG	CAG	CTG	GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	287
Leu	Gln	Leu	Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	
	80				85					90					95	
GTG	CTG	GAA	GAG	TAC	GAC	TGG	AGC	GGC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	335
Val	Leu	Glu	Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	
				100					105					110		
CAC	CCG	GGC	CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	GGC	GGC	GTC	GCC	GAC	383
His	Pro	Gly	His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	
			115					120					125			
GGC	AGC	CAC	GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	431
Ala	Ser	His	Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	
		130					135					140				
GAC	CCG	GGA	GGG	CCG	CGC	GGC	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	479
Asp	Pro	Gly	Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	
	145					150					155					
GAC	GGC	CCC	GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	527
Asp	Ala	Pro	Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	
	160				165				170						175	
CTC	TTC	GCC	GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	575
Leu	Phe	Ala	Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	
				180					185					190		
TGG	CTG	GTG	CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	623
Trp	Leu	Val	Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	
			195					200					205			
ACC	TTC	CCC	GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	671
Thr	Phe	Pro	Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	
		210					215						220			
AGC	CTG	CGC	CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	719
Ser	Leu	Arg	Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	
	225					230					235					
GGC	CAC	AGC	TAC	TGG	CGC	CAG	CAT	GGA	ACC	CAG	AAG	GGG	GTG	TGC	CAG	767
Ala	His	Ser	Tyr	Trp	Arg	Gln	His	Gly	Thr	Gln	Lys	Gly	Val	Cys	Gln	
	240				245					250					255	
CCC	GGG	CCG	GGG	ACT	GCC	GTG	TTC	ACC	CTG	GGC	CCG	TCA	GCC	CTG	CCC	815
Pro	Arg	Pro	Gly	Thr	Ala	Val	Phe	Thr	Leu	Gly	Pro	Ser	Ala	Leu	Pro	
				260					265						270	

GGG	AGG	CCT	TCT	ACA	GGC	ACC	TAC	TGA	ATG	TCA	CCT	GGG	AGG	GCC	GAG	863
Gly	Arg	Pro	Ser	Thr	Gly	Thr	Tyr	*	Met	Ser	Pro	Gly	Arg	Ala	Glu	
			275					280							285	
ACT	TCT	CCT	TCA	GCC	CTG	GTG	GGT	ACC	TGG	TCC	AGC	CCA	CCA	TGG	TGG	911
Thr	Ser	Pro	Ser	Ala	Leu	Val	Gly	Thr	Trp	Ser	Ser	Pro	Pro	Trp	Trp	
			290					295						300		
TGA	TCG	CCC	TCA	ACC	GGC	ACC	GCC	TCT	GGG	AGA	TGG	TGG	GGC	GCT	GGG	959
*	Ser	Pro	Ser	Thr	Gly	Thr	Ala	Ser	Gly	Arg	Trp	Trp	Gly	Ala	Gly	
	305						310					315				
AGC	ATG	GCG	TCC	TAT	ACA	TGA	AGT	ACC	CCG	TGT	GGC	CTC	GCT	ACA	GTG	1007
Ser	Met	Ala	Ser	Tyr	Thr	*	Ser	Thr	Pro	Cys	Gly	Leu	Ala	Thr	Val	
320					325					330					335	
CCT	CTC	TGC	AGC	CTG	TGG	TGG	ACA	GTC	GGC	ACC	TGA	CGG	TGG	CCA	CGC	1055
Pro	Leu	Cys	Ser	Leu	Trp	Trp	Thr	Val	Gly	Thr	*	Arg	Trp	Pro	Arg	
				340					345					350		
TGG	AAG	AGC	GGC	CCT	TTG	TCA	TCG	TGG	AGA	GCC	CTG	ACC	CTG	GCA	CAG	1103
Trp	Lys	Ser	Gly	Pro	Leu	Ser	Ser	Trp	Arg	Ala	Leu	Thr	Leu	Ala	Gln	
			355					360						365		
GAG	GCT	GTG	TCC	CCA	ACA	CCG	TGC	CCT	GCC	GCA	GGC	AGA	GCA	ACC	ACA	1151
Glu	Ala	Val	Ser	Pro	Thr	Pro	Cys	Pro	Ala	Ala	Gly	Arg	Ala	Thr	Thr	
		370					375					380				
CCT	TCA	GCA	GCG	GGG	ACG	TGG	CCC	CCT	ACA	CCA	AGC	TCT	GCT	GTA	AGG	1199
Pro	Ser	Ala	Ala	Gly	Thr	Trp	Pro	Pro	Thr	Pro	Ser	Ser	Ala	Val	Arg	
		385				390					395					
GAT	TCT	GCA	TCG	ACA	TCC	TCA	AGA	AGC	TGG	CCA	GAG	TGG	TCA	AAT	TCT	1247
Asp	Ser	Ala	Ser	Thr	Ser	Ser	Arg	Ser	Trp	Pro	Glu	Trp	Ser	Asn	Ser	
400				405					410					415		
CCT	ACG	ACC	TGT	ACC	TGG	TGA	CCA	ACG	GCA	AGC	ATG	GCA	AGC	GGG	TGC	1295
Pro	Thr	Thr	Cys	Thr	Trp	*	Pro	Thr	Ala	Ser	Met	Ala	Ser	Gly	Cys	
			420						425					430		
GCG	GCG	TAT	GGA	ACG	GCA	TGA	TTG	GGG	AGG	TGT	ACT	ACA	AGC	GGG	CAG	1343
Ala	Ala	Tyr	Gly	Thr	Ala	*	Leu	Gly	Arg	Cys	Thr	Thr	Ser	Gly	Gln	
		435					440						445			
ACA	TGG	CCA	TCG	GCT	CCC	TCA	CCA	TCA	ATG	AGG	AAC	GCT	CCG	AGA	TCG	1391
Thr	Trp	Pro	Ser	Ala	Pro	Ser	Pro	Ser	Met	Arg	Asn	Ala	Pro	Arg	Ser	
		450				455						460				
TAG	ACT	TCT	CTG	TAC	CCT	TTG	TGG	AGA	CGG	GCA	TCA	GTG	TGA	TGG	TGG	1439
*	Thr	Ser	Leu	Tyr	Pro	Leu	Trp	Arg	Arg	Ala	Ser	Val	*	Trp	Trp	
	465					470					475					
CTC	GCA	GCA	ATG	GCA	CCG	TCT	CCC	CCT	CGG	CCT	TCT	TGG	AGC	CAT	ATA	1487
Leu	Ala	Ala	Met	Ala	Pro	Ser	Pro	Pro	Arg	Pro	Ser	Trp	Ser	His	Ile	
480				485					490						495	
GCC	CTG	CAG	TGT	GGG	TGA	TGA	TGT	TTG	TCA	TGT	GCC	TCA	CTG	TGG	TGG	1535
Ala	Leu	Gln	Cys	Gly	*	*	Cys	Leu	Ser	Cys	Ala	Ser	Leu	Trp	Trp	
			500					505						510		
CCA	TCA	CCG	TCT	TCA	TGT	TCG	AGT	ACT	TCA	GCC	CTG	TCA	GCT	ACA	ACC	1583
Pro	Ser	Pro	Ser	Ser	Cys	Ser	Ser	Thr	Ser	Ala	Leu	Ser	Ala	Thr	Thr	
			515					520					525			
AGA	ACC	TCA	CCA	GAG	GCA	AGA	CTT	TCA	CTA	TCG	GCA	AGT	CCG	TGT	GGC	1631
Arg	Thr	Ser	Pro	Glu	Ala	Arg	Leu	Ser	Leu	Ser	Ala	Ser	Pro	Cys	Gly	
		530					535					540				

TGC	TGT	GGG	CGG	TGG	TCT	TCA	ACA	ACT	CAG	TGC	CCA	TCG	AGA	ACC	CGC	1679
Cys	Cys	Gly	Arg	Trp	Ser	Ser	Thr	Thr	Gln	Cys	Pro	Ser	Arg	Thr	Arg	
545						550					555					
GGG	GCA	CCA	CCA	GCA	AGA	TCA	TGG	TTC	TGG	TCT	GGG	CCT	TCT	TTG	CTG	1727
Gly	Ala	Pro	Pro	Ala	Arg	Ser	Trp	Phe	Trp	Ser	Gly	Pro	Ser	Leu	Leu	
560					565					570					575	
TCA	TCT	TCC	TCG	CCA	GAT	ACA	CGG	CCA	ACC	TGG	CCG	CCT	TCA	TGA	TCC	1775
Ser	Ser	Ser	Ser	Pro	Asp	Thr	Arg	Pro	Thr	Trp	Pro	Pro	Ser	*	Ser	
				580						585				590		
AAG	AGC	AAT	ACA	TCG	ACA	CTG	TGT	CGG	GCC	TCA	GTG	ACA	AGA	AGT	TTC	1823
Lys	Ser	Asn	Thr	Ser	Thr	Leu	Cys	Arg	Ala	Ser	Val	Thr	Arg	Ser	Phe	
			595					600					605			
AGC	GGC	CTC	AAG	ATC	AGT	ACC	CAC	CTT	TCC	GCT	TCG	GCA	CGG	TGC	CCA	1871
Ser	Gly	Leu	Lys	Ile	Ser	Thr	His	Leu	Ser	Ala	Ser	Ala	Arg	Cys	Pro	
		610					615						620			
ACG	GCA	GCA	CGG	AGC	GGA	ACA	TCC	GCA	GTA	ACT	ACC	GTG	ACA	TGC	ACA	1919
Thr	Ala	Ala	Arg	Ser	Gly	Thr	Ser	Ala	Val	Thr	Thr	Val	Thr	Cys	Thr	
		625				630						635				
CCC	ACA	TGG	TCA	AGT	TCA	ACC	AGC	GCT	CGG	TGG	AGG	ACG	CGC	TCA	CCA	1967
Pro	Thr	Trp	Ser	Ser	Ser	Thr	Ser	Ala	Arg	Trp	Arg	Thr	Arg	Ser	Pro	
640					645					650					655	
GCC	TCA	AGA	TGG	GGA	AGC	TGG	ATG	CCT	TCA	TCT	ATG	ATG	CTG	CTG	TCC	2015
Ala	Ser	Arg	Trp	Gly	Ser	Trp	Met	Pro	Ser	Ser	Met	Met	Leu	Leu	Ser	
				660					665					670		
TCA	ACT	ACA	TGG	CAG	GCA	AGG	ACG	AGG	GCT	GCA	AGC	TGG	TCA	CCA	TTG	2063
Ser	Thr	Thr	Trp	Gln	Ala	Arg	Thr	Arg	Ala	Ala	Ser	Trp	Ser	Pro	Leu	
			675					680					685			
GGT	CTG	GCA	AGG	TCT	TTG	CTA	CCA	CTG	GCT	ACG	GCA	TCG	CCA	TGC	AGA	2111
Gly	Leu	Ala	Arg	Ser	Leu	Leu	Pro	Leu	Ala	Thr	Ala	Ser	Pro	Cys	Arg	
		690					695					700				
AGG	ACT	CCC	ACT	GGA	AGC	GGG	CCA	TAG	ACC	TGG	CGC	TCT	TGC	AGT	TCC	2159
Arg	Thr	Pro	Thr	Gly	Ser	Gly	Pro	*	Thr	Trp	Arg	Ser	Cys	Ser	Ser	
	705					710					715					
TGG	GGG	ACG	GAG	AGA	CAC	AGA	AAC	TGG	AGA	CAG	TGT	GGC	TCT	CAG	GGA	2207
Trp	Gly	Thr	Glu	Arg	His	Arg	Asn	Trp	Arg	Gln	Cys	Gly	Ser	Gln	Gly	
	720				725					730					735	
TCT	GCC	AGA	ATG	AGA	AGA	ACG	AGG	TGA	TGA	GCA	GCA	AGC	TGG	ACA	TCG	2255
Ser	Ala	Arg	Met	Arg	Arg	Thr	Arg	*	*	Ala	Ala	Ser	Trp	Thr	Ser	
				740					745					750		
ACA	ACA	TGG	GAG	GCG	TCT	TCT	ACA	TGC	TGC	TGG	TGG	CCA	TGG	GGC	TGG	2303
Thr	Thr	Trp	Glu	Ala	Ser	Ser	Thr	Cys	Cys	Trp	Trp	Pro	Trp	Gly	Trp	
			755					760					765			
CCC	TGC	TGG	TCT	TCG	CCT	GGG	AGC	ACC	TGG	TCT	ACT	GGA	AGC	TGC	GCC	2351
Pro	Cys	Trp	Ser	Ser	Pro	Gly	Ser	Thr	Trp	Ser	Thr	Gly	Ser	Cys	Ala	
		770				775						780				
ACT	CGG	TGC	CCA	ACT	CAT	CCC	AGC	TGG	ACT	TCC	TGC	TGG	CTT	TCA	GCA	2399
Thr	Arg	Cys	Pro	Thr	His	Pro	Ser	Trp	Thr	Ser	Cys	Trp	Leu	Ser	Ala	
	785					790					795					
GGG	GCA	TCT	ACA	GCT	GCT	TCA	GCG	GGG	TGC	AGA	GCC	TCG	CCA	GCC	CAC	2447
Gly	Ala	Ser	Thr	Ala	Ala	Ser	Ala	Gly	Cys	Arg	Ala	Ser	Pro	Ala	His	
800					805					810					815	

CGC	GGC	AGG	CCA	GCC	CGG	ACC	TCA	GGG	CCA	GCT	CGG	CCC	AGG	CCA	GCG	2485
Arg	Gly	Arg	Pro	Ala	Arg	Thr	Ser	Arg	Pro	Ala	Arg	Pro	Arg	Pro	Ala	
				820					825						830	
TGC	TCA	AGA	TTC	TGC	AGG	CAG	CCC	GGG	ACA	TGG	TGA	CCA	CGG	CGG	GCG	2543
Cys	Ser	Arg	Phe	Cys	Arg	Gln	Pro	Ala	Thr	Trp	*	Pro	Arg	Arg	Ala	
			835					840					845			
TAA	GCA	ACT	CCC	TGG	ACC	GCG	CCA	CTC	GCA	CCA	TCG	AGA	ATT	GGG	GTG	2591
*	Ala	Thr	Pro	Trp	Thr	Ala	Pro	Leu	Ala	Pro	Ser	Arg	Ile	Gly	Val	
		850					855					860				
GCG	GCC	GCC	GTG	CGC	CCC	CAC	CGT	CCC	CCT	GCC	CGA	CCC	CGC	GGT	CTG	2639
Ala	Ala	Ala	Val	Arg	Pro	His	Arg	Pro	Pro	Ala	Arg	Pro	Arg	Gly	Leu	
	865					870					875					
GCC	CCA	GCC	CAT	GCC	TGC	CCA	CCC	CCG	ACC	CGC	CCC	CAG	AGC	CGA	GCC	2687
Ala	Pro	Ala	His	Ala	Cys	Pro	Pro	Pro	Thr	Arg	Pro	Gln	Ser	Arg	Ala	
880					885					890					895	
CCA	CGG	GCT	GGG	GAC	CGC	CAG	ACG	GGG	GTC	GCG	CGG	CGC	TTG	TGC	GCA	2735
Pro	Arg	Ala	Gly	Asp	Arg	Gln	Thr	Gly	Val	Ala	Arg	Arg	Leu	Cys	Ala	
				900					905					910		
GGG	CTC	CGC	AGC	CCC	CGG	GCC	GCC	CCC	CGA	CGC	CGG	GGC	CGC	CCC	TGT	2783
Gly	Leu	Arg	Ser	Pro	Arg	Ala	Ala	Pro	Arg	Arg	Arg	Gly	Arg	Pro	Cys	
			915					920					925			
CCG	ACG	TCT	CCC	GAG	TGT	CGC	GCC	GCC	CAG	CCT	GGG	AGG	CGC	GGT	GGC	2831
Pro	Thr	Ser	Pro	Glu	Cys	Arg	Ala	Ala	Gln	Pro	Gly	Arg	Arg	Gly	Gly	
		930					935					940				
CGG	TGC	GGA	CCG	GGC	ACT	GCG	GGA	GGC	ACC	TCT	CGG	CCT	CCG	AGC	GGC	2879
Arg	Cys	Gly	Pro	Gly	Thr	Ala	Gly	Gly	Thr	Ser	Arg	Pro	Pro	Ser	Gly	
	945					950					955					
CCC	TGT	CGC	CCG	CGC	GCT	GTC	ACT	ACA	GCT	CCT	TTC	CTC	GAG	CCG	ACC	2927
Pro	Cys	Arg	Pro	Arg	Ala	Val	Thr	Thr	Ala	Pro	Phe	Leu	Glu	Pro	Thr	
960					965					970					975	
GAT	CCG	GCC	GCC	CCT	TCC	TCC	CGC	TCT	TCC	CGG	AGC	CCC	CGG	AGC	TGG	2975
Asp	Pro	Ala	Ala	Pro	Ser	Ser	Arg	Ser	Ser	Arg	Ser	Pro	Arg	Ser	Trp	
				980						985					990	
AGG	ACC	TGC	CGC	TGC	TCG	GTC	CGG	AGC	AGC	TGG	CCC	GGC	GGG	AGG	CCC	3023
Arg	Thr	Cys	Arg	Cys	Ser	Val	Arg	Ser	Ser	Trp	Pro	Gly	Gly	Arg	Pro	
			995				1000					1005				
TGC	TGA	ACG	CGG	CCT	GGG	CCC	GGG	GCT	CGC	GCC	CGA	GTC	ACG	CTT	CCC	3071
Cys	*	Thr	Arg	Pro	Gly	Pro	Gly	Ala	Arg	Ala	Arg	Val	Thr	Leu	Pro	
	1010					1015						1020				
TGC	CCA	GCT	CCG	TGG	CCG	AGG	CCT	TCG	CTC	GGC	CCA	GCT	CGC	TGC	CCG	3119
Cys	Pro	Ala	Pro	Trp	Pro	Arg	Pro	Ser	Leu	Gly	Pro	Ala	Arg	Cys	Pro	
	1025				1030						1035					
CTG	GGT	GCA	CCG	GCC	CCG	CCT	GCG	CCC	GCC	CCG	ACG	GCC	ACT	CGG	CCT	3167
Leu	Gly	Ala	Pro	Ala	Pro	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Arg	Pro	
1040				1045				1050						1055		
GCA	GGC	GCT	TGG	CGC	AGG	CGC	AGT	CGA	TGT	GCT	TGC	CGA	TCT	ACC	GGG	3215
Ala	Gly	Ala	Trp	Arg	Arg	Arg	Ser	Arg	Cys	Ala	Cys	Arg	Ser	Thr	Gly	
			1060					1065					1070			
AGG	CCT	GCC	AGG	AGG	GCG	AGC	AGG	CAG	GGG	CCC	CCG	CCT	GGC	AGC	ACA	3263
Arg	Pro	Ala	Arg	Arg	Ala	Ser	Arg	Gln	Gly	Pro	Pro	Pro	Gly	Ser	Thr	
		1075					1080					1085				

GAC AGC ACG TCT GCC TGC ACG CCC ACG CCC ACC TGC CAT TGT GCT GGG Asp Ser Thr Ser Ala Cys Thr Pro Thr Pro Thr Cys His Cys Ala Gly 1090 1095 1100	3311
GGG CTG TCT GTC CTC ACC TTC CAC CCT GTG ACA GCC ACG GCT CCT GGC Gly Leu Ser Val Leu Thr Phe His Pro Val Thr Ala Thr Ala Pro Gly 1105 1110 1115	3359
TCT CCG GCG CCT GGG GGC CTC TGG GGC ACA GCG GCA GGA CTC TGG GGC Ser Pro Ala Pro Gly Gly Leu Trp Gly Thr Ala Ala Gly Leu Trp Gly 1120 1125 1130 1135	3407
TGG GCA CAG GCT ACA GAG ACA GTG GGG GAC TGG ACG AGA TCA GCA GTG Trp Ala Gln Ala Thr Glu Thr Val Gly Asp Trp Thr Arg Ser Ala Val 1140 1145 1150	3455
TAG CCC GTG GGA CGC AAG GCT TCC CGG GAC CCT GCA CCT GGA GAC GGA * Pro Val Gly Arg Lys Ala Ser Arg Asp Pro Ala Pro Gly Asp Gly 1155 1160 1165	3503
TCT CCA GTC TGG AGT CAG AAG TGT GAG TTA TCA GCC ACT CAG GCT CCG Ser Pro Val Trp Ser Gln Lys Cys Glu Leu Ser Ala Thr Gln Ala Pro 1170 1175 1180	3551
AGC CAG CTG GAT TCT CTG CCT GCC ACT GTC AGG GTT AAG CGG CAG GCA Ser Gln Leu Asp Ser Leu Pro Ala Thr Val Arg Val Lys Arg Gln Ala 1185 1190 1195	3599
GGA TTG GCC CTT CTC TGG CTT CTA CCA TGA AAT CCT GGC CAT GGC ACC Gly Leu Ala Leu Leu Trp Leu Leu Pro * Asn Pro Gly His Gly Thr 1200 1205 1210 1215	3647
CCA GTG ACA GAT GAT GTC TTC CAT GGT CAT CAG TGA CCT CAG CTA GCC Pro Val Thr Asp Asp Val Phe His Gly His Gln * Pro Gln Leu Ala 1220 1225 1230	3695
TCA Ser	3698

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...3243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC GAG GCG Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala 1 5 10 15	48
GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG CCC AAC Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn 20 25 30	96
CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC GTG GGC	144

Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly		
	35						40					45					
CTC	ATC	AGC	GTC	GTG	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	CAG	AAC	192	
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys		
	50					55					60						
GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	TAC	TGG	240	
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp		
	65				70					75					80		
CGC	CAG	CAT	GGA	ACC	CAG	AAG	GGG	GTG	TGC	CAG	CCC	CGG	CCG	GGG	ACT	288	
Arg	Gln	His	Gly	Thr	Gln	Lys	Gly	Val	Cys	Gln	Pro	Arg	Pro	Gly	Thr		
				85					90					95			
GCC	GTG	TTC	ACC	CTG	GGC	CCG	TCA	GCC	CTG	CCC	GGG	AGG	CCT	TCT	ACA	336	
Ala	Val	Phe		Leu	Gly	Pro	Ser	Ala	Leu	Pro	Gly	Arg		Ser	Thr		
			100					105					110				
GGC	ACC	TAC	TGA	ATG	TCA	CCT	GGG	AGG	GCC	GAG	ACT	TCT	CCT	TCA	GCC	384	
Gly	Thr	Tyr	*	Met	Ser	Pro	Gly	Arg	Ala	Glu	Thr	Ser	Pro	Ser	Ala		
		115					120					125					
CTG	GTG	GGT	ACC	TGG	TCC	AGC	CCA	CCA	TGG	TGG	TGA	TCG	CCC	TCA	ACC	432	
Leu	Val	Gly	Thr	Trp	Ser	Ser	Pro	Pro	Trp	Trp	*	Ser	Pro	Ser	Thr		
	130					135					140						
GGC	ACC	GCC	TCT	GGG	AGA	TGG	TGG	GGC	GCT	GGG	AGC	ATG	GCG	TCC	TAT	480	
Gly	Thr	Ala	Ser	Gly	Arg	Trp	Trp	Gly	Ala	Gly	Ser	Met	Ala	Ser	Tyr		
	145				150					155					160		
ACA	TGA	AGT	ACC	CCG	TGT	GGC	CTC	GCT	ACA	GTG	CCT	CTC	TGC	AGC	CTG	528	
Thr	*	Ser	Thr	Pro	Cys	Gly	Leu	Ala	Thr	Val	Pro	Leu	Cys	Ser	Leu		
				165					170					175			
TGG	TGG	ACA	GTC	GGC	ACC	TGA	CGG	TGG	CCA	CGC	TGG	AAG	AGC	GGC	CCT	576	
Trp	Trp	Thr	Val	Gly	Thr	*	Arg	Trp	Pro	Arg	Trp	Lys	Ser	Gly	Pro		
			180					185					190				
TTG	TCA	TCG	TGG	AGA	GCC	CTG	ACC	CTG	GCA	CAG	GAG	GCT	GTG	TCC	CCA	624	
Leu	Ser	Ser	Trp	Arg	Ala	Leu	Thr	Leu	Ala	Gln	Glu	Ala	Val	Ser	Pro		
			195				200						205				
ACA	CCG	TGC	CCT	GCC	GCA	GGC	AGA	GCA	ACC	ACA	CCT	TCA	GCA	GCG	GGG	672	
Thr	Pro	Cys	Pro	Ala	Ala	Gly	Arg	Ala	Thr	Thr	Pro	Ser	Ala	Ala	Gly		
	210					215					220						
ACG	TGG	CCC	CCT	ACA	CCA	AGC	TCT	GCT	GTA	AGG	GAT	TCT	GCA	TCG	ACA	720	
Thr	Trp	Pro	Pro	Thr	Pro	Ser	Ser	Ala	Val	Arg	Asp	Ser	Ala	Ser	Thr		
	225				230					235					240		
TCC	TCA	AGA	AGC	TGG	CCA	GAG	TGG	TCA	AAT	TCT	CCT	ACG	ACC	TGT	ACC	768	
Ser	Ser	Arg	Ser	Trp	Pro	Glu	Trp	Ser	Asn	Ser	Pro	Thr	Thr	Cys	Thr		
				245					250					255			
TGG	TGA	CCA	ACG	GCA	AGC	ATG	GCA	AGC	GGG	TGC	GCG	GCG	TAT	GGA	ACG	816	
Trp	*	Pro	Thr	Ala	Ser	Met	Ala	Ser	Gly	Cys	Ala	Ala	Tyr	Gly	Thr		
			260				265						270				
GCA	TGA	TTG	GGG	AGG	TGT	ACT	ACA	AGC	GGG	CAG	ACA	TGG	CCA	TCG	GCT	864	
Ala	*	Leu	Gly	Arg	Cys	Thr	Thr	Ser	Gly	Gln	Thr	Pro	Ser	Ala			
		275					280					285					
CCC	TCA	CCA	TCA	ATG	AGG	AAC	GCT	CCG	AGA	TCG	TAG	ACT	TCT	CTG	TAC	912	
Pro	Ser	Pro	Ser	Met	Arg	Asn	Ala	Pro	Arg	Ser	*	Thr	Ser	Leu	Tyr		
	290					295					300						



CCT	TTG	TGG	AGA	GGG	GCA	TCA	GTG	TGA	TGG	TGG	CTC	GCA	GCA	ATG	GCA	960
Pro	Leu	Trp	Arg	Arg	Ala	Ser	Val	*	Trp	Trp	Leu	Ala	Ala	Met	Ala	
305					310					315					320	
CCG	TCT	CCC	CCT	GGG	GGT	TCT	TGG	AGC	CAT	ATA	GCC	CTG	CAG	TGT	GGG	1008
Pro	Ser	Pro	Pro	Arg	Pro	Ser	Trp	Ser	His	Ile	Ala	Leu	Gln	Cys	Gly	
				325					330					335		
TGA	TGA	TGT	TTG	TCA	TGT	GCC	TCA	CTG	TGG	TGG	CCA	TCA	CCG	TCT	TCA	1056
*	*	Cys	Leu	Ser	Cys	Ala	Ser	Leu	Trp	Trp	Pro	Ser	Pro	Ser	Ser	
			340					345					350			
TGT	TCG	AGT	ACT	TCA	GCC	CTG	TCA	GCT	ACA	ACC	AGA	ACC	TCA	CCA	GAG	1104
Cys	Ser	Ser	Thr	Ser	Ala	Leu	Ser	Ala	Thr	Thr	Arg	Thr	Ser	Pro	Glu	
		355					360					365				
GCA	AGA	AGT	CCG	GGG	GCC	CAG	CTT	TCA	CTA	TCG	GCA	AGT	CCG	TGT	GGC	1152
Ala	Arg	Ser	Pro	Gly	Ala	Gln	Leu	Ser	Leu	Ser	Ala	Ser	Pro	Cys	Gly	
	370				375						380					
TGC	TGT	GGG	CGC	TGG	TCT	TCA	ACA	ACT	CAG	TGC	CCA	TCG	AGA	ACC	CGC	1200
Cys	Cys	Gly	Arg	Trp	Ser	Ser	Thr	Thr	Gln	Cys	Pro	Ser	Arg	Thr	Arg	
385				390					395						400	
GGG	GCA	CCA	CCA	GCA	AGA	TCA	TGG	TTC	TGG	TCT	GGG	CCT	TCT	TTG	CTG	1248
Gly	Ala	Pro	Pro	Ala	Arg	Ser	Trp	Phe	Trp	Ser	Gly	Pro	Ser	Leu	Leu	
				405				410						415		
TCA	TCT	TCC	TCG	CCA	GAT	ACA	CGG	CCA	ACC	TGG	CCG	CCT	TCA	TGA	TCC	1296
Ser	Ser	Ser	Ser	Pro	Asp	Thr	Arg	Pro	Thr	Trp	Pro	Pro	Ser	*	Ser	
			420					425					430			
AAG	AGC	AAT	ACA	TCG	ACA	CTG	TGT	CGG	GCC	TCA	GTG	ACA	AGA	AGT	TTC	1344
Lys	Ser	Asn	Thr	Ser	Thr	Leu	Cys	Arg	Ala	Ser	Val	Thr	Arg	Ser	Phe	
		435				440					445					
AGC	GGC	CTC	AAG	ATC	AGT	ACC	CAC	CTT	TCC	GCT	TCG	GCA	CGG	TGC	CCA	1392
Ser	Gly	Leu	Lys	Ile	Ser	Thr	His	Leu	Ser	Ala	Ser	Ala	Arg	Cys	Pro	
	450				455						460					
ACG	GCA	GCA	CGG	AGC	GGA	ACA	TCC	GCA	GTA	ACT	ACC	GTG	ACA	TGC	ACA	1440
Thr	Ala	Ala	Arg	Ser	Gly	Thr	Ser	Ala	Val	Thr	Thr	Val	Thr	Cys	Thr	
465				470					475					480		
CCC	ACA	TGG	TCA	AGT	TCA	ACC	AGC	GCT	CGG	TGG	AGG	ACG	CGC	TCA	CCA	1488
Pro	Thr	Trp	Ser	Ser	Ser	Thr	Ser	Ala	Arg	Trp	Arg	Thr	Arg	Ser	Pro	
				485				490						495		
GCC	TCA	AGA	TGG	GCT	CTG	AGG	CTC	AGC	CTG	TCC	CCA	GGA	AGC	TGG	ATG	1536
Ala	Ser	Arg	Trp	Ala	Leu	Arg	Leu	Ser	Leu	Ser	Pro	Gly	Ser	Trp	Met	
			500					505					510			
CCT	TCA	TCT	ATG	ATG	CTG	CTG	TCC	TCA	ACT	ACA	TGG	CAG	GCA	AGG	ACG	1584
Pro	Ser	Ser	Met	Met	Leu	Leu	Ser	Ser	Thr	Thr	Trp	Gln	Ala	Arg	Thr	
		515					520					525				
AGG	GCT	GCA	AGC	TGG	TCA	CCA	TTG	GGT	CTG	GCA	AGG	TCT	TTG	CTA	CCA	1632
Arg	Ala	Ala	Ser	Trp	Ser	Pro	Leu	Gly	Leu	Ala	Arg	Ser	Leu	Leu	Pro	
	530					535					540					
CTG	GCT	ACG	GCA	TCG	CCA	TGC	AGA	AGG	ACT	CCC	ACT	GGA	AGC	GGG	CCA	1680
Leu	Ala	Thr	Ala	Ser	Pro	Cys	Arg	Arg	Thr	Pro	Thr	Gly	Ser	Gly	Pro	
545				550					555					560		
TAG	ACC	TGG	CGC	TCT	TGC	AGT	TCC	TGG	GGG	ACG	GAG	AGA	CAC	AGA	AAC	1728
*	Thr	Trp	Arg	Ser	Cys	Ser	Ser	Trp	Gly	Thr	Glu	Arg	His	Arg	Asn	
				565					570					575		

TGG	AGA	CAG	TGT	GGC	TCT	CAG	GGA	TCT	GCC	AGA	ATG	AGA	AGA	ACG	AGG	1776
Trp	Arg	Gln	Cys	Gly	Ser	Gln	Gly	Ser	Ala	Arg	Met	Arg	Arg	Thr	Arg	
		580						585					590			
TGA	TGA	GCA	GCA	AGC	TGG	ACA	TCG	ACA	ACA	TGG	GAG	GCG	TCT	TCT	ACA	1824
*	*	Ala	Ala	Ser	Trp	Thr	Ser	Thr	Thr	Trp	Glu	Ala	Ser	Ser	Thr	
		595					600				605					
TGC	TGC	TGG	TGG	CCA	TGG	GGC	TGG	CCC	TGC	TGG	TCT	TCG	CCT	GGG	AGC	1872
Cys	Cys	Trp	Trp	Pro	Trp	Gly	Trp	Pro	Cys	Trp	Ser	Ser	Pro	Gly	Ser	
	610					615					620					
ACC	TGG	TCT	ACT	GGA	AGC	TGC	GCC	ACT	CGG	TGC	CCA	ACT	CAT	CCC	AGC	1920
Thr	Trp	Ser	Thr	Gly	Ser	Cys	Ala	Thr	Arg	Cys	Pro	Thr	His	Pro	Ser	
625				630						635					640	
TGG	ACT	TCC	TGC	TGG	CTT	TCA	GCA	GGG	GCA	TCT	ACA	GCT	GCT	TCA	GCG	1968
Trp	Thr	Ser	Cys	Trp	Leu	Ser	Ala	Gly	Ala	Ser	Thr	Ala	Ala	Ser	Ala	
			645					650						655		
GGG	TGC	AGA	GCC	TCG	CCA	GCC	CAC	CGC	GGC	AGG	CCA	GCC	CGG	ACC	TCA	2016
Gly	Cys	Arg	Ala	Ser	Pro	Ala	His	Arg	Gly	Arg	Pro	Ala	Arg	Thr	Ser	
			660					665					670			
CGG	CCA	GCT	CGG	CCC	AGG	CCA	GCG	TGC	TCA	AGA	TTC	TGC	AGG	CAG	CCC	2064
Arg	Pro	Ala	Arg	Pro	Arg	Pro	Ala	Cys	Ser	Arg	Phe	Cys	Arg	Gln	Pro	
		675					680					685				
GCG	ACA	TGG	TGA	CCA	CGG	CGG	GCG	TAA	GCA	ACT	CCC	TGG	ACC	GCG	CCA	2112
Ala	Thr	Trp	*	Pro	Arg	Arg	Ala	*	Ala	Thr	Pro	Trp	Thr	Ala	Pro	
	690					695					700					
CTC	GCA	CCA	TCG	AGA	ATT	GCG	GTG	GCG	GCC	GCC	GTG	CGC	CCC	CAC	CGT	2160
Leu	Ala	Pro	Ser	Arg	Ile	Gly	Val	Ala	Ala	Ala	Val	Arg	Pro	His	Arg	
705					710					715					720	
CCC	CCT	GCC	CGA	CCC	CGC	GGT	CTG	GCC	CCA	GCC	CAT	GCC	TGC	CCA	CCC	2208
Pro	Pro	Ala	Arg	Pro	Arg	Gly	Leu	Ala	Pro	Ala	His	Ala	Cys	Pro	Pro	
				725				730						735		
CCG	ACC	CGC	CCC	CAG	AGC	CGA	GCC	CCA	CGG	GCT	GGG	GAC	CGC	CAG	ACG	2256
Pro	Thr	Arg	Pro	Gln	Ser	Arg	Ala	Pro	Arg	Ala	Gly	Asp	Arg	Gln	Thr	
			740					745					750			
GGG	GTC	GCG	CGG	CGC	TTG	TGC	GCA	GGG	CTC	CGC	AGC	CCC	CGG	GCC	GCC	2304
Gly	Val	Ala	Arg	Arg	Leu	Cys	Ala	Gly	Leu	Arg	Ser	Pro	Arg	Ala	Ala	
		755					760					765				
CCC	CGA	CGC	CGG	GGC	CGC	CCC	TGT	CCG	ACG	TCT	CCC	GAG	TGT	CGC	GCC	2352
Pro	Arg	Arg	Arg	Gly	Arg	Pro	Cys	Pro	Thr	Ser	Pro	Glu	Cys	Arg	Ala	
		770				775					780					
GCC	CAG	CCT	GGG	AGG	CGC	GGT	GGC	CGG	TGC	GGA	CCG	GGC	ACT	GCG	GGA	2400
Ala	Gln	Pro	Gly	Arg	Arg	Gly	Gly	Arg	Cys	Gly	Pro	Gly	Thr	Ala	Gly	
785					790				795						800	
GGC	ACC	TCT	CGG	CCT	CGG	AGC	GGC	CCC	TGT	CGC	CCG	CGC	GCT	GTC	ACT	2448
Gly	Thr	Ser	Arg	Pro	Pro	Ser	Gly	Pro	Cys	Arg	Pro	Arg	Ala	Val	Thr	
				805				810						815		
ACA	GCT	CCT	TTC	CTC	GAG	CGG	ACC	GAT	CCG	GCC	GCC	CCT	TCC	TCC	CGC	2496
Thr	Ala	Pro	Phe	Leu	Glu	Pro	Thr	Asp	Pro	Ala	Ala	Pro	Ser	Ser	Arg	
			820					825					830			
TCT	TCC	CGG	AGC	CCC	CGG	AGC	TGG	AGG	ACC	TGC	CGC	TGC	TCG	GTC	CGG	2544
Ser	Ser	Arg	Ser	Pro	Arg	Ser	Trp	Arg	Thr	Cys	Arg	Cys	Ser	Val	Arg	
		835					840					845				

AGC AGC TGG CCC GGC GGG AGG CCC TGC TGA ACG CGG CCT GGG CCC GGG	2592
Ser Ser Trp Pro Gly Gly Arg Pro Cys * Thr Arg Pro Gly Pro Gly	
850 855 860	
GCT CGC GCC CGA GTC ACG CTT CCC TGC CCA GCT CGG TGG CCG AGG CCT	2640
Ala Arg Ala Arg Val Thr Leu Pro Cys Pro Ala Pro Trp Pro Arg Pro	
865 870 875 880	
TCG CTC GGC CCA GCT CGC TGC CCG CTG GGT GCA CCG GCC CCG CCT GCG	2688
Ser Leu Gly Pro Ala Arg Cys Pro Leu Gly Ala Pro Ala Pro Pro Ala	
885 890 895	
CCC GCC CCG ACG GCC ACT CGG CCT GCA GGC GCT TGG CGC AGG CGC AGT	2736
Pro Ala Pro Thr Ala Thr Arg Pro Ala Gly Ala Trp Arg Arg Arg Ser	
900 905 910	
CGA TGT GCT TGC CGA TCT ACC GGG AGG CCT GCC AGG AGG GCG AGC AGG	2784
Arg Cys Ala Cys Arg Ser Thr Gly Arg Pro Ala Arg Arg Ala Ser Arg	
915 920 925	
CAG GGG CCC CCG CCT GGC AGC ACA GAC AGC ACG TCT GCC TGC ACG CCC	2832
Gln Gly Pro Pro Pro Gly Ser Thr Asp Ser Thr Ser Ala Cys Thr Pro	
930 935 940	
ACG CCC ACC TGC CAT TGT GCT GGG GGG CTG TCT GTC CTC ACC TTC CAC	2880
Thr Pro Thr Cys His Cys Ala Gly Gly Leu Ser Val Leu Thr Phe His	
945 950 955 960	
CCT GTG ACA GCC ACG GCT CCT GGC TCT CCG GCG CCT GGG GGC CTC TGG	2928
Pro Val Thr Ala Thr Ala Pro Gly Ser Pro Ala Pro Gly Gly Leu Trp	
965 970 975	
GGC ACA GCG GCA GGA CTC TGG GGC TGG GCA CAG GCT ACA GAG ACA GTG	2976
Gly Thr Ala Ala Gly Leu Trp Gly Trp Ala Gln Ala Thr Glu Thr Val	
980 985 990	
GGG GAC TGG ACG AGA TCA GCA GTG TAG CCC GTG GGA CCG AAG GCT TCC	3024
Gly Asp Trp Thr Arg Ser Ala Val * Pro Val Gly Arg Lys Ala Ser	
995 1000 1005	
CGG GAC CCT GCA CCT GGA GAC GGA TCT CCA GTC TGG AGT CAG AAG TGT	3072
Arg Asp Pro Ala Pro Gly Asp Gly Ser Pro Val Trp Ser Gln Lys Cys	
1010 1015 1020	
GAG TTA TCA GCC ACT CAG GCT CCG AGC CAG CTG GAT TCT CTG CCT GCC	3120
Glu Leu Ser Ala Thr Gln Ala Pro Ser Gln Leu Asp Ser Leu Pro Ala	
1025 1030 1035 1040	
ACT GTC AGG GTT AAG CGG CAG GCA GGA TTG GCC CTT CTC TGG CTT CTA	3168
Thr Val Arg Val Lys Arg Gln Ala Gly Leu Ala Leu Leu Trp Leu Leu	
1045 1050 1055	
CCA TGA AAT CCT GGC CAT GGC ACC CCA GTG ACA GAT GAT GTC TTC CAT	3216
Pro * Asn Pro Gly His Gly Thr Pro Val Thr Asp Asp Val Phe His	
1060 1065 1070	
GGT CAT CAG TGA CCT CAG CTA GCC TCA	3243
Gly His Gln * Pro Gln Leu Ala Ser	
1075 1080	

(2) INFORMATION FOR SEQ ID NO:45:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4092 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTTAATAA GATTTCGNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CCG GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806

Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195					200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
		240				245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
255					260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
335					340					345					350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
		400				405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
					420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			

AAG Lys	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTG Val	AAA Lys	TTC Phe	TTC Ser	TAC Tyr	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val	1622
		465					470					475				
ACC Thr	AAC Asn	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys	CGG Arg	GTG Val	GGG Arg	GGG Gly	GTA Val	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
	480					485					490					
ATT Ile	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu	1718
	495				500					505					510	
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro	TTT Phe	1766
				515					520					525		
GTG Val	GAG Glu	ACG Thr	GGC Gly	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly	ACC Thr	GTC Val	1814
			530					535					540			
TCC Ser	CCC Pro	TCG Ser	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro	TAT Tyr	AGC Ser	CCT Pro	GCA Ala	GTG Val	TGG Trp	GTG Val	ATG Met	1862
		545					550					555				
ATG Met	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
	560					565					570					
GAG Glu	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys	1958
	575				580				585						590	
AAG Lys	TCC Ser	GGG Gly	GGC Gly	CCA Pro	GCT Ala	TTC Phe	ACT Thr	ATC Ile	GGC Gly	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu	CTG Leu	2006
				595					600					605		
TGG Trp	GCG Ala	CTG Leu	GTC Val	TTC Phe	AAC Asn	AAC Asn	TCA Ser	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro	CGG Arg	GGC Gly	2054
			610					615					620			
ACC Thr	ACC Thr	AGC Ser	AAG Lys	ATC Ile	ATG Met	GTT Val	CTG Leu	GTG Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val	ATC Ile	2102
		625					630					635				
TTC Phe	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	ACG Thr	GCC Ala	AAC Asn	CTG Leu	GCC Ala	GCC Ala	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	2150
	640					645					650					
CAA Gln	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	GTG Val	TGG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg	2198
	655				660					665					670	
CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr	CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn	GGC Gly	2246
				675					680					685		
AGC Ser	ACG Thr	GAG Glu	CGG Arg	AAC Asn	ATC Ile	CGC Arg	AGT Ser	AAC Asn	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His	ACC Thr	CAC His	2294
			690					695					700			
ATG Met	GTG Val	AAG Lys	TTC Phe	AAC Asn	CAG Gln	CGC Arg	TGG Ser	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu	ACC Thr	AGC Ser	CTC Leu	2342
		705					710					715				
AAG Lys	ATG Met	GGC Gly	TCT Ser	GAG Glu	GCT Ala	CAG Gln	CCT Pro	GTG Val	CCC Pro	AGG Arg	AAG Lys	CTG Leu	GAT Asp	GCC Ala	TTC Phe	2390
	720					725					730					

ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	2438
Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	
735					740					745					750	
TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	2486
Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	
				755					760					765		
TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	2534
Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	
			770					775					780			
CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	2582
Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	
		785					790					795				
ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	2630
Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	
	800					805					810					
AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	ATG	CTG	2678
Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	
815					820					825					830	
CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	GAG	CAC	CTG	2726
Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	
				835					840					845		
GTC	TAC	TGG	AAG	CTG	CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	2774
Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	
			850					855					860			
TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	2822
Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	
		865					870					875				
CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	CTC	ACC	GCC	2870
Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	
	880					885					890					
AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	GCC	CGC	GAC	2918
Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	
	895				900					905					910	
ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	2966
Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	
				915					920					925		
ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	TCC	CCC	3014
Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	
			930					935					940			
TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	3062
Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	
		945					950					955				
CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	3110
Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	
	960					965				970						
CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	3158
Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	
	975				980					985					990	
ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TGG	CGC	CGC	CCA	3206
Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	
				995				1000						1005		

GCC TGG GAG GCG CGG TGG CCG GTG CCG ACC GGG CAC TGC GGG AGG CAC	3254
Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His	
1010 1015 1020	
CTC TCG GCG TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC	3302
Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser	
1025 1030 1035	
TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG CTC TTC	3350
Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe	
1040 1045 1050	
CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG GAG CAG	3398
Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln	
1055 1060 1065 1070	
CTG GCC CCG CCG GAG GCC CTG CTG AAC GCG GCC TGG GCC CCG GGC TCG	3446
Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser	
1075 1080 1085	
CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC TTC GCT	3494
Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala	
1090 1095 1100	
CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC GCC CGC	3542
Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg	
1105 1110 1115	
CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG TCG ATG	3590
Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met	
1120 1125 1130	
TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG GCA GGG	3638
Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly	
1135 1140 1145 1150	
GCC CCC GCG TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC CAC GCC	3686
Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala	
1155 1160 1165	
CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA CCC TGT	3734
His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys	
1170 1175 1180	
GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG GGC CAC	3782
Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His	
1185 1190 1195	
AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT GGC GGA	3830
Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly	
1200 1205 1210	
CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC CCC GGA	3878
Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly	
1215 1220 1225 1230	
CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA	3930
Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val	
1235 1240 124	
GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAA3CGGCAG	3990
GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA	4050
GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4092



(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1244 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Gly	Ala	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Leu	Phe	Gly	1	5	10	15
Ala	Trp	Ala	Gly	Leu	Gly	Pro	Gly	Gln	Gly	Glu	Gln	Gly	Met	Thr	Val	20	25	30	
Ala	Val	Val	Phe	Ser	Ser	Ser	Gly	Pro	Pro	Gln	Ala	Gln	Phe	Arg	Val	35	40	45	
Arg	Leu	Thr	Pro	Gln	Ser	Phe	Leu	Asp	Leu	Pro	Leu	Glu	Ile	Gln	Pro	50	55	60	
Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	Ser	Leu	Leu	Thr	Gln	65	70	75	
Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	Gly	Ile	Val	Phe	Glu	85	90	95	
Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser	100	105	110	
Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	Ala	Val	115	120	125	
Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	Gly	Val	130	135	140	
Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	Glu	Tyr	145	150	155	
Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	His	Ala	165	170	175	
Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	Val	Ser	180	185	190	
Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	Gly	Pro	195	200	205	
Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	Val	Phe	210	215	220	
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala	225	230	235	
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn	245	250	255	
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	260	265	270	
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	275	280	285	
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp				



645										650					655				
Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln				
			660					665						670					
Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr				
		675					680						685						
Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val				
	690					695					700								
Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met				
	705				710						715				720				
Gly	Ser	Glu	Ala	Gln	Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr				
				725					730					735					
Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys				
			740					745					750						
Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly				
		755					760						765						
Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala				
	770					775					780								
Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val				
	785				790				795						800				
Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser				
			805						810					815					
Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val				
			820					825					830						
Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr				
		835					840					845							
Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu				
	850					855					860								
Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser				
	865				870						875				880				
Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser				
			885						890					895					
Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val				
		900						905					910						
Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile				
		915					920					925							
Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro				
	930					935						940							
Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro				
	945				950						955				960				
Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala				
			965						970					975					
Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro				
		980						985						990					
Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp				

995	1000	1005
Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser 1010 1015 1020		
Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe 1025 1030 1035 1040		
Pro Arg Ala Asp Arg Ser G Arg Pro Phe Leu Pro Leu Phe Pro Glu 1045 1050 1055		
Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala 1060 1065 1070		
Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro 1075 1080 1085		
Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro 1090 1095 1100		
Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp 1105 1110 1115 1120		
Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu 1125 1130 1135		
Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro 1140 1145 1150		
Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala His Leu 1155 1160 1165		
Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser 1170 1175 1180		
His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly 1185 1190 1195 1200		
Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp 1205 1210 1215		
Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys 1220 1225 1230		
Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1235 1240		

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4053 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCCTTAATAA GATTTGACNAC GTACACTCGA GCCATCGCGA GTGTCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCGG GCCTAAAAAT ACCCGGAAC TACAGCCCG AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CCG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	
GGG CCG CGC GCG CGC ACC CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC	854
Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	
210 215 220	
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC	902
Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	
225 230 235	

GAG Glu 240	GCG Ala 240	GCG Ala 240	CAG Gln 240	GCC Ala 240	GGT Gly 240	CTG Leu 245	GTG Val 245	GGG Gly 245	CCC Pro 250	CCC Gly 250	CAC His 250	GTG Val 250	TGG Trp 250	CTG Leu 250	GTG Val 250	950
CCC Pro 255	AAC Asn 255	CTG Leu 255	GCG Ala 255	CTG Leu 255	GGC Gly 260	AGC Ser 260	ACC Thr 260	GGT Asp 260	GGG Ala 265	CCC Pro 265	CCC Pro 265	GCC Ala 265	ACC Thr 265	TTC Phe 270	CCC Pro 270	998
GTG Val 275	GCG Gly 275	CTC Leu 275	ATC Ile 275	AGC Ser 275	GTC Val 275	GTC Val 275	ACC Thr 275	GAG Glu 280	AGC Ser 280	TGG Trp 280	GCG Arg 280	CTC Leu 280	AGC Ser 280	CTG Leu 285	CGC Arg 285	1046
CAG Gln 290	AAG Lys 290	GTG Val 290	GCG Arg 290	GAC Asp 290	GGC Gly 290	GTG Val 290	GCC Ala 295	ATT Ile 295	CTG Leu 295	GCC Ala 295	CTG Leu 295	GGC Gly 300	GCC Ala 300	CAC His 300	AGC Ser 300	1094
TAC Tyr 305	TGG Trp 305	GCG Arg 305	CAG Gln 305	CAT His 305	GGA Gly 305	ACC Thr 310	CTG Leu 310	CCA Pro 310	GCC Ala 310	CCG Pro 310	GCC Ala 315	GGG Gly 315	GAC Asp 315	TGC Cys 315	CGT Arg 315	1142
GTT Val 320	CAC His 320	CCT Pro 320	GGG Gly 320	CCC Pro 320	GTC Val 325	AGC Ser 325	CCT Pro 325	GGC Ala 325	CGG Arg 325	GAG Glu 330	GCC Ala 330	TTC Phe 330	TAC Tyr 330	AGG Arg 330	CAC His 330	1190
CTA Leu 335	CTG Leu 335	AAT Asn 335	GTC Val 335	ACC Thr 335	TGG Trp 340	GAG Glu 340	GGC Gly 340	CGA Arg 340	GAC Asp 345	TTC Phe 345	TCC Ser 345	TTC Phe 345	AGC Ser 345	CCT Pro 345	GGT Gly 350	1238
GGG Gly 355	TAC Tyr 355	CTG Leu 355	GTC Val 355	CAG Gln 355	CCC Pro 355	ACC Thr 355	ATG Met 355	GTG Val 360	GTG Val 360	ATC Ile 360	GCC Ala 360	CTC Leu 360	AAC Asn 365	CGG Arg 365	CAC His 365	1286
CGC Arg 370	CTC Leu 370	TGG Trp 370	GAG Glu 370	ATG Met 370	GTG Val 370	GGG Gly 370	CGC Arg 375	TGG Trp 375	GAG Glu 375	CAT His 375	GGC Gly 375	GTC Val 375	CTA Leu 380	TAC Tyr 380	ATG Met 380	1334
AAG Lys 385	TAC Tyr 385	CCC Pro 385	GTG Val 385	TGG Trp 385	CCT Pro 385	CGC Arg 385	TAC Tyr 390	AGT Ser 390	GCC Ala 390	TCT Ser 390	CTG Leu 395	CAG Gln 395	CCT Pro 395	GTG Val 395	GTG Val 395	1382
GAC Asp 400	AGT Ser 400	CGG Arg 400	CAC His 400	CTG Leu 400	ACG Thr 405	GTG Val 405	GCC Ala 405	AGG Thr 405	CTG Leu 410	GAA Glu 410	GAG Glu 410	CGG Arg 410	CCC Pro 410	TTT Phe 410	GTC Val 410	1430
ATC Ile 415	GTG Val 415	GAG Glu 415	AGC Ser 415	CCT Pro 415	GAC Asp 420	CCT Pro 420	GGC Gly 420	ACA Thr 420	GGA Gly 425	GGC Gly 425	TGT Cys 425	GTC Val 425	CCC Pro 425	AAC Asn 425	ACC Thr 430	1478
GTG Val 435	CCC Pro 435	TGC Cys 435	CGC Arg 435	AGG Arg 435	CAG Gln 435	AGC Ser 435	AAC Asn 440	CAC His 440	ACC Thr 440	TTC Phe 440	AGC Ser 440	AGC Ser 440	GGG Gly 445	GAC Asp 445	GTG Val 445	1526
GCC Ala 450	CCC Pro 450	TAC Tyr 450	ACC Thr 450	AAG Lys 450	CTC Leu 450	TGC Cys 450	TGT Cys 455	AAG Lys 455	GGA Gly 455	TTC Phe 455	TGC Cys 455	ATC Ile 460	GAC Asp 460	ATC Ile 460	CTC Leu 460	1574
AAG Lys 465	AAG Lys 465	CTG Leu 465	GCC Ala 465	AGA Arg 465	GTG Val 465	GTC Val 465	AAA Lys 470	TTC Phe 470	TCC Ser 470	TAC Tyr 470	GAC Asp 475	CTG Leu 475	TAC Tyr 475	CTG Leu 475	GTG Val 475	1622
ACC Thr 480	AAC Asn 480	GGC Gly 480	AAG Lys 480	CAT His 480	GGC Gly 485	AAG Lys 485	CGG Arg 485	GTG Val 485	CGC Arg 485	GGC Gly 490	GTA Val 490	TGG Trp 490	AAC Asn 490	GGC Gly 490	ATG Met 490	1670
ATT Ile 495	GGG Gly 495	GAG Glu 495	GTG Val 495	TAC Tyr 495	TAC Tyr 500	AAG Lys 500	CGG Arg 500	GCA Ala 500	GAC Asp 505	ATG Met 505	GCC Ala 505	ATC Ile 505	GGC Gly 505	TCC Ser 505	CTC Leu 510	1713

ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
			515						520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTG	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
	575				580				585						590	
ACT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	TGG	GCG	CTG	GTC	TTC	2006
Thr	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	
				595					600					605		
AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	ACC	ACC	AGC	AAG	ATC	2054
Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	
			610					615					620			
ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	TTC	CTC	GCC	AGA	TAC	2102
Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	
		625					630						635			
ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	CAA	TAC	ATC	GAC	ACT	2150
Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	
	640					645						650				
GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	CCT	CAA	GAT	CAG	TAC	2198
Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	
	655				660				665						670	
CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	AGC	ACG	GAG	CGG	AAC	2246
Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	
			675					680						685		
ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	ATG	GTC	AAG	TTC	AAC	2294
Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	
			690				695						700			
CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	AAG	ATG	GGG	AAG	CTG	2342
Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Leu	
		705					710					715				
GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	TAC	ATG	GCA	GGC	AAG	2390
Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	
	720					725						730				
GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	GGC	AAG	GTC	TTT	GCT	2438
Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	
	735				740				745						750	
ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	2486
Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	
				755				760						765		
GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	2534
Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	
			770					775					780			

AAA	CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	2582
Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	
		785					790					795				
GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	2630
Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	
	800					805					810					
TAC	ATG	CTG	CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	2678
Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	
815					820					825					830	
GAG	CAC	CTG	GTC	TAC	TGG	AAG	CTG	CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	2726
Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	
				835					840					845		
CAG	CTG	GAC	TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	2774
Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	
			850					855					860			
AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	2822
Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	
		865					870					875				
CTC	ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	2870
Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	
	880					885					890					
GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	GCG	GTA	AGC	AAC	TCC	CTG	GAC	CGC	2918
Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	
	895				900					905					910	
GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	GCT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	2966
Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	
				915					920					925		
CCG	TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	3014
Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	
			930					935					940			
ACC	CCC	GAC	CCG	CCC	CCA	GAG	GGG	AAG	CCC	ACG	GGC	TGG	GGA	CCG	CCA	3062
Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	
		945					950					955				
GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	3110
Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	
	960					965				970						
CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	3158
Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	
	975				980					985					990	
CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	3206
Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	
				995					1000					1005		
GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	3254
Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	
			1010					1015					1020			
CAC	TAC	AGC	TCC	TTT	CCT	CGA	GGG	GAC	CGA	TCC	GGC	CGC	CCC	TTC	CTC	3302
His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	Arg	Pro	Phe	Leu	
			1025					1030				1035				
CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG	CTG	GAG	GAC	CTG	CCG	CTG	CTC	GGT	3350
Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	Pro	Leu	Leu	Gly	
	1040						1045				1050					



CCG GAG CAG CTG GCC CGG CGG GAG GCG CTG CTG AAC GCG GCC TGG GCC Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala 1055 1060 1065 1070	3398
CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu 1075 1080 1085	3446
GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala 1090 1095 1100	3494
TGC GCC CGC CCC GAC GGC CAC TCG GCG TGC AGG CGC TTG GCG CAG GCG Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala 1105 1110 1115	3542
CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu 1120 1125 1130	3590
CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His 1135 1140 1145 1150	3638
GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu 1155 1160 1165	3686
CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro 1170 1175 1180	3734
CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp 1185 1190 1195	3782
AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly 1200 1205 1210	3830
TTC CCG GGA CCC TGC ACC TGG AGA CCG ATC TCC AGT CTG GAG TCA GAA Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu 1215 1220 1225 1230	3878
GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA Val	3931
CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCTTCTCTG GCTTCTACCA TGAAATCCTG	3991
GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT	4051
CA	4053

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly

1	5	10	15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val	20	25	30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val	35	40	45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro	50	55	60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln	65	70	75
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu	85	90	95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser	100	105	110
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val	115	120	125
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val	130	135	140
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr	145	150	155
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala	165	170	175
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser	180	185	190
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro	195	200	205
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe	210	215	220
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala	225	230	235
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn	245	250	255
Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly	260	265	270
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys	275	280	285
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp	290	295	300
Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His	305	310	315
Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu	325	330	335
Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr	340	345	350
Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu			

355	360	365
Trp Glu Met Val Gly Arg	Trp Glu His Gly Val	Leu Tyr Met Lys Tyr
370	375	380
Pro Val Trp Pro Arg Tyr	Ser Ala Ser Leu Gln	Pro Val Val Asp Ser
385	390	395
Arg His Leu Thr Val Ala Thr	Leu Glu Glu Arg	Pro Phe Val Ile Val
405	410	415
Glu Ser Pro Asp Pro Gly Thr	Gly Gly Cys Val	Pro Asn Thr Val Pro
420	425	430
Cys Arg Arg Gln Ser Asn His	Thr Phe Ser Ser	Gly Asp Val Ala Pro
435	440	445
Tyr Thr Lys Leu Cys Cys Lys	Gly Phe Cys Ile	Asp Ile Leu Lys Lys
450	455	460
Leu Ala Arg Val Val Lys Phe	Ser Tyr Asp Leu Tyr	Leu Val Thr Asn
465	470	475
Gly Lys His Gly Lys Arg Val	Arg Gly Val Trp	Asn Gly Met Ile Gly
485	490	495
Glu Val Tyr Tyr Lys Arg Ala	Asp Met Ala Ile	Gly Ser Leu Thr Ile
500	505	510
Asn Glu Glu Arg Ser Glu Ile	Val Asp Phe Ser Val	Pro Phe Val Glu
515	520	525
Thr Gly Ile Ser Val Met Val	Ala Arg Ser Asn	Gly Thr Val Ser Pro
530	535	540
Ser Ala Phe Leu Glu Pro Tyr	Ser Pro Ala Val	Trp Val Met Met Phe
545	550	555
Val Met Cys Leu Thr Val Val	Ala Ile Thr Val	Phe Met Phe Glu Tyr
565	570	575
Phe Ser Pro Val Ser Tyr Asn	Gln Asn Leu Thr	Arg Gly Lys Thr Phe
580	585	590
Thr Ile Gly Lys Ser Val Trp	Leu Leu Trp Ala	Leu Val Phe Asn Asn
595	600	605
Ser Val Pro Ile Glu Asn Pro	Arg Gly Thr Thr	Ser Lys Ile Met Val
610	615	620
Leu Val Trp Ala Phe Phe Ala	Val Ile Phe Leu	Ala Arg Tyr Thr Ala
625	630	635
Asn Leu Ala Ala Phe Met Ile	Gln Glu Gln Tyr	Ile Asp Thr Val Ser
645	650	655
Gly Leu Ser Asp Lys Lys Phe	Gln Arg Pro Gln	Asp Gln Tyr Pro Pro
660	665	670
Phe Arg Phe Gly Thr Val Pro	Asn Gly Ser Thr	Glu Arg Asn Ile Arg
675	680	685
Ser Asn Tyr Arg Asp Met His	Thr His Met Val	Lys Phe Asn Gln Arg
690	695	700
Ser Val Glu Asp Ala Leu Thr	Ser Leu Lys Met	Gly Lys Leu Asp Ala

705		710		715		720
Phe Ile Tyr Asp	Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu	725	730	735		
Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr		740	745	750		
Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile		755	760	765		
Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu		770	775	780		
Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val		785	790	795		800
Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met		805	810	815		
Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His		820	825	830		
Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu		835	840	845		
Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly		850	855	860		
Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr		865	870	875		880
Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg		885	890	895		
Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr		900	905	910		
Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser		915	920	925		
Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro		930	935	940		
Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly		945	950	955		960
Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro		965	970	975		
Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg		980	985	990		
Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg		995	1000	1005		
His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr		1010	1015	1020		
Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu		1025	1030	1035		1040
Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu		1045	1050	1055		
Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly						

1060	1065	1070
Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe 1075 1080 1085		
Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala 1090 1095 1100		
Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser 1105 1110 1115 1120		
Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala 1125 1130 1135		
Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His 1140 1145 1150		
Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro 1155 1160 1165		
Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly 1170 1175 1180		
His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly 1185 1190 1195 1200		
Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro 1205 1210 1215		
Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1220 1225 1230		

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4017 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 189..3848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	240
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	300
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	360
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	

35																40				45				
CGT	GTC	CGC	CTC	ACC	CCC	CAG	AGC	TTC	CTG	GAC	CTA	CCC	CTG	GAG	ATC	374								
Arg	Val	Arg	Leu	Thr	Pro	Gln	Ser	Phe	Leu	Asp	Leu	Pro	Leu	Glu	Ile									
			50					55					60											
CAG	CCG	CTC	ACA	GTT	GGG	GTC	AAC	ACC	ACC	AAC	CCC	AGC	AGC	CTC	CTC	422								
Gln	Pro	Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	Ser	Leu	Leu									
		65					70					75												
ACC	CAG	ATC	TGC	GGC	CTC	CTG	GGT	GCT	GCC	CAC	GTC	CAC	GGC	ATT	GTC	470								
Thr	Gln	Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	Gly	Ile	Val									
	80					85					90													
TTT	GAG	GAC	AAC	GTG	GAC	ACC	GAG	GCG	GTG	GCC	CAG	ATC	CTT	GAC	TTC	518								
Phe	Glu	Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe									
	95				100					105					110									
ATC	TCC	TCC	CAG	ACC	CAT	GTG	CCC	ATC	CTC	AGC	ATC	AGC	GGA	GGC	TCT	566								
Ile	Ser	Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser									
				115					120					125										
GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	CTG	CAG	CTG	614								
Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu									
			130					135					140											
GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	GTG	CTG	GAA	662								
Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu									
		145					150					155												
GAG	TAC	GAC	TGG	AGC	GCC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	CAC	CCG	GGC	710								
Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly									
	160					165					170													
CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	CGC	GCC	GTC	GCC	GAC	GCC	AGC	CAC	758								
His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His									
	175				180					185					190									
GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	GAC	CCG	GGA	806								
Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly									
				195					200					205										
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854								
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro									
			210					215					220											
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902								
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala									
		225					230					235												
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950								
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val									
	240					245					250													
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998								
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro									
	255				260					265					270									
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046								
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg									
				275					280					285										
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094								
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser									
			290					295					300											
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142								

Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
	335				340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
	400					405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
	415				420					425					430	
GTG	CCC	TGG	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				
ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
	480					485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
	495				500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TGG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					

GAG Glu 575	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val 580	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn 585	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys 590	1998
AAG Lys	TCC Ser	GGG Gly	GGC Gly	CCA Pro 595	GCT Ala	TTC Phe	ACT Thr	ATC Ile	GGC Gly 600	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu 605	CTG Leu	2006
TGG Trp	GCG Ala	CTG Leu	GTC Val 610	TTC Phe	AAC Asn	AAC Asn	TCA Ser	GTG Val 615	CCC Pro	ATC Ile	GAG Glu	AAC Asn 620	CCG Pro	CGG Arg	GGC Gly	2054
ACC Thr	ACC Thr	AGC Ser 625	AAG Lys	ATC Ile	ATG Met	GTT Val	CTG Leu 630	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe 635	GCT Ala	GTC Val	ATC Ile	2102
TTC Phe 640	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	ACG Thr	GCC Ala 645	AAC Asn	CTG Leu	GCC Ala	GCC Ala 650	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	2150
CAA Gln 655	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	GTG Val 660	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp 665	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg 670	2198
CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr 675	CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe 680	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn 685	GGC Gly	2246
AGC Ser	ACG Thr	GAG Glu	CGG Arg 690	AAC Asn	ATC Ile	CGC Arg	AGT Ser 695	AAC Asn	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His 700	ACC Thr	CAC His	2294
ATG Met	GTC Val	AAG Lys 705	TTC Phe	AAC Asn	CAG Gln	CGC Arg	TCG Ser 710	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu 715	ACC Thr	AGC Ser	CTC Leu	2342
AAG Lys 720	ATG Met	GGC Gly	AAG Lys	GAC Asp	GAG Glu	GGC Gly 725	TGC Cys	AAG Lys	CTG Leu	GTC Val 730	ACC Thr	ATT Ile	GGG Gly	TCT Ser	GGC Gly	2390
AAG Lys 735	GTC Val	TTT Phe	GCT Ala	ACC Thr	ACT Thr 740	GGC Gly	TAC Tyr	GGC Gly	ATC Ile	GCC Ala 745	ATG Met	CAG Gln	AAG Lys	GAC Asp	TCC Ser 750	2438
CAC His	TGG Trp	AAG Lys	CGG Arg	GCC Ala 755	ATA Ile	GAC Asp	CTG Leu	GCG Ala 760	CTC Leu	TTG Leu	CAG Gln	TTC Phe	CTG Leu	GGG Gly 765	GAC Asp	2486
GGA Gly	GAG Glu	ACA Thr	CAG Gln 770	AAA Lys	CTG Leu	GAG Glu	ACA Thr 775	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly 780	ATC Ile	TGC Cys	CAG Gln	2534
AAT Asn	GAG Glu	AAG Lys 785	AAC Asn	GAG Glu	GTG Val	ATG Met	AGC Ser 790	AGC Ser	AAG Lys	CTG Leu	GAC Asp 795	ATC Ile	GAC Asp	AAC Asn	ATG Met	2582
GGA Gly 800	GGC Gly	GTC Val	TTC Phe	TAC Tyr	ATG Met 805	CTG Leu	CTG Leu	GTG Val	GCC Ala	ATG Met 810	GGG Gly	CTG Leu	GCC Ala	CTG Leu	CTG Leu	2630
GTC Val 815	TTC Phe	GCC Ala	TGG Trp	GAG Glu	CAC His 820	CTG Leu	GTC Val	TAC Tyr	TGG Trp	AAG Lys 825	CTG Leu	CGC Arg	CAC His	TCG Ser	GTG Val 830	2678
CCC Pro	AAC Asn	TCA Ser	TCC Ser	CAG Gln 835	CTG Leu	GAC Asp	TTC Phe	CTG Leu	CTG Leu 840	GCT Ala	TTC Phe	AGC Ser	AGG Arg	GGC Gly 845	ATC Ile	2726



TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	2774
Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	
			850					855					860			
GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	2822
Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	
		865						870					875			
ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	AAC	2870
Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	
	880						885					890				
TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	CGC	2918
Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	
	895				900					905					910	
CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	2966
Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	
				915					920					925		
CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	GGC	3014
Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	
			930						935					940		
TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	3062
Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	
		945					950					955				
CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	3110
Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	
	960					965					970					
TCC	GGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	CGG	3158
Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	
	975				980				985						990	
ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	TCG	3206
Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	
				995					1000					1005		
CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	CCT	CGA	GCC	GAC	CGA	TCC	GGC	3254
Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	
			1010					1015					1020			
CGC	CCC	TTC	CTC	CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG	CTG	GAG	GAC	CTG	3302
Arg	Pro	Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	
		1025					1030					1035				
CCG	CTG	CTC	GGT	CCG	GAG	CAG	CTG	GCC	CGG	CGG	GAG	GCC	CTG	CTG	AAC	3350
Pro	Leu	Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	
	1040					1045					1050					
GCG	GCC	TGG	GCC	CGG	GGC	TCG	CGC	CCG	AGT	CAC	GCT	TCC	CTG	CCC	AGC	3398
Ala	Ala	Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	Ser	Leu	Pro	Ser	
	1055				1060				1065						1070	
TCC	GTG	GCC	GAG	GCC	TTC	GCT	CGG	CCC	AGC	TCG	CTG	CCC	GCT	GGG	TGC	3446
Ser	Val	Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	Pro	Ala	Gly	Cys	
			1075						1080					1085		
ACC	GGC	CCC	GCC	TGC	GCC	CGC	CCC	GAC	GGC	CAC	TCG	GCC	TGC	AGG	CGC	3494
Thr	Gly	Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	Ala	Cys	Arg	Arg	
		1090						1095					1100			
TTG	GGC	CAG	GCG	CAG	TCG	ATG	TGC	TTG	CCG	ATC	TAC	CGG	GAG	GCC	TGC	3542
Leu	Ala	Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	Arg	Glu	Ala	Cys	
	1105						1110					1115				

CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAG Gln Glu Gly Gln Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His 1120 1125 1130	3590
GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val 1135 1140 1145 1150	3638
TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly 1155 1160 1165	3686
GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr 1170 1175 1180	3734
GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg 1185 1190 1195	3782
GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser 1200 1205 1210	3830
CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT Leu Glu Ser Glu Val 1215 122	3885
CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA	3945
TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT	4005
CAGCTAGCCT CA	4017

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly 1 5 10 15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val 20 25 30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val 35 40 45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro 50 55 60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln 65 70 75 80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu 85 90 95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser 100 105 110

Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	Ala	Val
	115						120					125			
Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	Gly	Val
	130						135				140				
Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	Glu	Tyr
145					150					155					160
Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	His	Ala
				165					170					175	
Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	Val	Ser
			180					185					190		
Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	Gly	Pro
	195						200					205			
Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	Val	Phe
	210					215					220				
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala
225					230					235					240
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn
				245					250					255	
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly
			260					265					270		
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys
	275						280					285			
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp
	290					295					300				
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His
305					310					315					320
Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu
				325					330					335	
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr
			340					345					350		
Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu
	355						360					365			
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr
	370					375					380				
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser
385					390					395					400
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val
				405					410					415	
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro
			420					425					430		
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro
		435					440					445			
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys
	450					455					460				
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn

465		470		475		480
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly	485		490			495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile	500		505			510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu	515		520		525	
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro	530		535		540	
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe	545	550		555		560
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr	565		570			575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser	580		585		590	
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala	595		600		605	
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr	610		615		620	
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu	625	630		635		640
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr	645		650			655
Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln	660		665		670	
Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr	675		680		685	
Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val	690		695		700	
Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met	705		710		715	720
Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val	725		730			735
Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp	740		745		750	
Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu	755		760		765	
Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu	770		775		780	
Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly	785	790		795		800
Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe	805		810			815
Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn						

820					825					830					
Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser
		835					840					845			
Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser
	850					855					860				
Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu
	865					870					875				880
Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu
				885					890					895	
Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala
			900					905					910		
Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys
			915				920					925			
Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly
	930					935					940				
Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro
	945					950					955				960
Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg
				965					970					975	
Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly
			980					985					990		
His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala
		995					1000					1005			
Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	Arg	Pro
		1010				1015					1020				
Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	Pro	Leu
	1025					1030					1035				1040
Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	Ala	Ala
				1045					1050					1055	
Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	Ser	Leu	Pro	Ser	Ser	Val
			1060					1065					1070		
Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	Pro	Ala	Gly	Cys	Thr	Gly
			1075				1080					1085			
Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	Ala	Cys	Arg	Arg	Leu	Ala
	1090					1095					1100				
Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	Arg	Glu	Ala	Cys	Gln	Glu
	1105					1110					1115				1120
Gly	Glu	Gln	Ala	Gly	Ala	Pro	Ala	Trp	Gln	His	Arg	Gln	His	Val	Cys
				1125					1130					1135	
Leu	His	Ala	His	Ala	His	Leu	Pro	Leu	Cys	Trp	Gly	Ala	Val	Cys	Pro
			1140				1145						1150		
His	Leu	Pro	Pro	Cys	Asp	Ser	His	Gly	Ser	Trp	Leu	Ser	Gly	Ala	Trp
		1155					1160					1165			
Gly	Pro	Leu	Gly	His	Ser	Gly	Arg	Thr	Leu	Gly	Leu	Gly	Thr	Gly	Tyr

1170 1175 1180  
 Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr  
 1185 1190 1195 1200  
 Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu  
 1205 1210 1215  
 Ser Glu Val

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

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CCCTTAATAA GATTTGACAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG      60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC      120
CTATGAATTA TTTATGCGCG GCCTAAAAAT ACCCCGAAC TACAGCCCG AGTGACCTC      180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC      230
      Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu
        1             5             10

TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG      278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met
      15             20             25             30

ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC      326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe
              35             40             45

CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC      374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile
              50             55             60

CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC      422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu
              65             70             75

ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC      470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val
              80             85             90

TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC      518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe
              95             100             105             110

ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT      566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser
              115             120             125

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GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	CTG	CAG	CTG	614
Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	
			130						135					140		
GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	GTG	CTG	GAA	662
Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	
		145					150					155				
GAG	TAC	GAC	TGG	AGC	GCC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	CAC	CCG	GGC	710
Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	
	160					165					170					
CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	CGC	GCC	GTC	GCC	GAC	GCC	AGC	CAC	758
His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	
	175				180					185					190	
GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	GAC	CCG	GGA	806
Val	Ser	Trp	Arg	Leu	Asp	Val	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195					200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TGG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
	225						230					235				
GAG	GCG	GCG	CAG	GCC	GCT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
	240				245					250						
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
	255				260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275				280						285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
	335				340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355				360						365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				

GAC Asp	AGT Ser	CGG Arg	CAC His	CTG Leu	ACG Thr	GTG Val	GCC Ala	ACG Thr	CTG Leu	GAA Glu	GAG Glu	CGG Arg	CCC Pro	TTT Phe	GTC Val	1430
400						405					410					
ATC Ile	GTG Val	GAG Glu	AGC Ser	CCT Pro	GAC Asp	CCT Pro	GGC Gly	ACA Thr	GGA Gly	GGC Gly	TGT Cys	GTC Val	CCC Pro	AAC Asn	ACC Thr	1478
415					420					425					430	
GTG Val	CCC Pro	TGC Cys	CGC Arg	AGG Arg	CAG Gln	AGC Ser	AAC Asn	CAC His	ACC Thr	TTC Phe	AGC Ser	AGC Ser	GGG Gly	GAC Asp	GTG Val	1526
				435					440					445		
GCC Ala	CCC Pro	TAC Tyr	ACC Thr	AAG Lys	CTC Leu	TGC Cys	TGT Cys	AAG Lys	GGA Gly	TTC Phe	TGC Cys	ATC Ile	GAC Asp	ATC Ile	CTC Leu	1574
			450					455					460			
AAG Lys	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val	1622
		465					470				475					
ACC Thr	AAC Asn	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys	CGG Arg	GTG Val	CGC Arg	GGC Gly	GTA Val	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
480						485					490					
ATT Ile	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu	1718
495					500					505					510	
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro	TTT Phe	1766
				515					520					525		
GTG Val	GAG Glu	ACG Thr	GGC Gly	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly	ACC Thr	GTC Val	1814
			530					535					540			
TCC Ser	CCC Pro	TGC Ser	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro	TAT Tyr	AGC Ser	CCT Pro	GCA Ala	GTG Val	TGG Trp	GTG Val	ATG Met	1862
		545					550					555				
ATG Met	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
560						565					570					
GAG Glu	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys	1958
575					580					585					590	
ACT Thr	TTC Phe	ACT Thr	ATC Ile	GGC Gly	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu	CTG Leu	TGG Trp	GCG Ala	CTG Leu	GTC Val	TTC Phe	2006
				595					600					605		
AAC Asn	AAC Asn	TCA Ser	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro	CGG Arg	GGC Gly	ACC Thr	ACC Thr	AGC Ser	AAG Lys	ATC Ile	2054
			610					615					620			
ATG Met	GTT Val	CTG Leu	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val	ATC Ile	TTC Phe	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	2102
		625					630					635				
ACG Thr	GCC Ala	AAC Asn	CTG Leu	GCC Ala	GCC Ala	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	CAA Gln	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	2150
640					645						650					
GTG Val	TGC Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg	CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr	2198
655					660					665						670



CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	AGC	ACG	GAG	CGG	AAC	2246
Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	
				675					680					685		
ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	ATG	GTC	AAG	TTC	AAC	2294
Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	
			690					695					700			
CAG	CGC	TGG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	AAG	ATG	GGC	TCT	GAG	2342
Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Ser	Glu	
		705					710					715				
GCT	CA3	CCT	GTC	CCC	AGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	2390
Ala	Gln	Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
	720					725					730					
GTC	CTC	AAC	TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	2438
Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
	735				740					745					750	
ATT	GG3	TCT	GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	2486
Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	
				755					760					765		
CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	2534
Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
			770					775					780			
TTC	CT3	GGG	GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GT3	TGG	CTC	TCA	2582
Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	
		785					790					795				
GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	2630
Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	
	800					805					810					
ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	ATG	CTG	CTG	GT3	GCC	ATG	GGG	2678
Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	
	815				820					825					830	
CTG	GCC	CT3	CTG	GTC	TTC	GCC	TGG	GAG	CAC	CT3	GTC	TAC	TGG	AAG	CTG	2726
Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	
				835					840					845		
CGC	CAC	TC3	GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	TTC	CTG	CTG	GCT	TTC	2774
Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	
			850					855					860			
AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	2822
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	
		865					870					875				
CCA	CC3	CG3	CAG	GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TC3	GCC	CAG	GCC	2870
Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	
	880					885						890				
AGC	GT3	CTC	AAG	ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GT3	ACC	ACG	GCG	2918
Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	
	895				900					905					910	
GGC	STA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	2966
Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	
				915					920					925		
GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CC3	ACC	CC3	CGG	3014
Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	
			930					935					940			

TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG	3062
Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	
		945					950					955				
AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	3110
Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	
	960					965					970					
CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	3158
Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	
	975				980					985					990	
CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	3206
Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	
				995					1000						1005	
TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	3254
Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	
			1010					1015							1020	
CGG	CCC	CTG	TGG	CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	CCT	CGA	GCC	3302
Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	
		1025					1030						1035			
GAC	CGA	TCC	GGC	CGC	CCC	TTC	CTC	CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG	3350
Asp	Arg	Ser	Gly	Arg	Pro	Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	
	1040					1045					1050					
CTG	GAG	GAC	CTG	CCG	CTG	CTC	GGT	CCG	GAG	CAG	CTG	GCC	CGG	CGG	GAG	3398
Leu	Glu	Asp	Leu	Pro	Leu	Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	
	1055				1060					1065					1070	
GCC	CTG	CTG	AAC	GCG	GCC	TGG	GCC	CGG	GGC	TCG	CGC	CCG	AGT	CAC	GCT	3446
Ala	Leu	Leu	Asn	Ala	Ala	Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	
			1075						1080					1085		
TCC	CTG	CCC	AGC	TCC	GTG	GCC	GAG	GCC	TTC	GCT	CGG	CCC	AGC	TCG	CTG	3494
Ser	Leu	Pro	Ser	Ser	Val	Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	
			1090					1095						1100		
CCC	GCT	GGG	TGC	ACC	GGC	CCC	GCC	TGC	GCC	CGC	CCC	GAC	GGC	CAC	TCG	3542
Pro	Ala	Gly	Cys	Thr	Gly	Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	
		1105					1110					1115				
GCC	TGC	AGG	CGC	TTG	GCG	CAG	GCG	CAG	TCG	ATG	TGC	TTG	CCG	ATC	TAC	3590
Ala	Cys	Arg	Arg	Leu	Ala	Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	
	1120					1125					1130					
CGG	GAG	GCC	TGC	CAG	GAG	GGC	GAG	CAG	GCA	GGG	GCC	CCC	GCC	TGG	CAG	3638
Arg	Glu	Ala	Cys	Gln	Glu	Gly	Glu	Gln	Ala	Gly	Ala	Pro	Ala	Trp	Gln	
	1135				1140					1145					1150	
CAC	AGA	CAG	CAC	GTC	TGC	CTG	CAC	GCC	CAC	GCC	CAC	CTG	CCA	TTG	TGC	3686
His	Arg	Gln	His	Val	Cys	Leu	His	Ala	His	Ala	His	Leu	Pro	Leu	Cys	
				1155					1160					1165		
TGG	GGG	GCT	GTC	TGT	CCT	CAC	CTT	CCA	CCC	TGT	GAC	AGC	CAC	GGC	TCC	3734
Trp	Gly	Ala	Val	Cys	Pro	His	Leu	Pro	Pro	Cys	Asp	Ser	His	Gly	Ser	
			1170					1175						1180		
TGG	CTG	TCC	GGC	GCC	TGG	GGG	CCT	CTG	GGG	CAC	AGC	GGC	AGG	ACT	CTG	3782
Trp	Leu	Ser	Gly	Ala	Trp	Gly	Pro	Leu	Gly	His	Ser	Gly	Arg	Thr	Leu	
		1185					1190					1195				
GGG	CTG	GGC	ACA	GGC	TAC	AGA	GAC	AGT	GGG	GGA	CTG	GAC	GAG	ATC	AGC	3830
Gly	Leu	Gly	Thr	Gly	Tyr	Arg	Asp	Ser	Gly	Gly	Leu	Asp	Glu	Ile	Ser	
	1200					1205					1210					

AGT GTA GCG CGT GGA AAG GAA GGC TTC CCG GGA CCC TGC ACC TGG AGA	3873
Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg	
1215 1225 1230	
CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG	3925
Arg Ile Ser Ser Leu Glu Ser Glu Val	
1235 124	
CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG	3985
CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT	4045
TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4077

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly	1 5 10 15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val	20 25 30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val	35 40 45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro	50 55 60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln	65 70 75 80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu	85 90 95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser	100 105 110
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val	115 120 125
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val	130 135 140
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr	145 150 155 160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala	165 170 175
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser	180 185 190
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro	195 200 205
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe	210 215 220

Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala		
225					230					235					240		
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn		
				245					250					255			
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly		
			260					265					270				
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys		
		275					280					285					
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp		
	290					295					300						
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His		
305					310					315					320		
Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu		
				325					330					335			
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr		
			340					345					350				
Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu		
		355					360					365					
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr		
	370					375					380						
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser		
385					390					395				400			
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val		
				405					410					415			
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro		
			420					425					430				
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro		
			435				440					445					
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys		
	450					455					460						
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn		
465					470					475					480		
Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly		
				485					490					495			
Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile		
			500					505					510				
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu		
							520					525					
Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro		
	530					535					540						
Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe		
545					550					555					560		
Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr		
				565					570					575			

Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Thr	Phe
			580					585					590		
Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn
		595					600					605			
Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val
	610					615					620				
Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala
	625				630					635					640
Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser
				645					650					655	
Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro
			660					665					670		
Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg
		675					680					685			
Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg
	690					695					700				
Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Ser	Glu	Ala	Gln
	705				710					715					720
Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu
				725					730					735	
Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly
			740					745					750		
Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys
		755					760					765			
Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu
		770				775					780				
Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile
	785				790					795					800
Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp
				805					810					815	
Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala
			820					825					830		
Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His
		835					840					845			
Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg
		850				855					860				
Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro
	865				870				875						880
Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val
				885					890					895	
Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val
			900					905					910		
Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly
		915					920					925			

Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly  
930 935 940

Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro  
945 950 955 960

Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg  
965 970 975

Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser  
980 985 990

Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro  
995 1000 1005

Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro  
1010 1015 1020

Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg  
1025 1030 1035 1040

Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu  
1045 1050 1055

Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu  
1060 1065 1070

Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu  
1075 1080 1085

Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala  
1090 1095 1100

Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys  
1105 1110 1115 1120

Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu  
1125 1130 1135

Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg  
1140 1145 1150

Gln His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly  
1155 1160 1165

Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu  
1170 1175 1180

Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu  
1185 1190 1195 1200

Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val  
1205 1210 1215

Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile  
1220 1225 1230

Ser Ser Leu Glu Ser Glu Val  
1235

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4002 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 189..3833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCTTAATAA GATTTCGNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCGCGGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAAC TACAGCCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCT TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	

GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTG	ACG	GTG	GAA	CTG	GAC	CCG	GGA	806
Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195					200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGG	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
		240				245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GGG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
255					260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	GGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
		320				325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
335					340					345					350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
		400				405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
415					420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			



AAG Lys	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val	1622
		465					470					475				
ACC Thr	AAC Asn	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys	CGG Arg	GTG Val	CGC Arg	GGC Gly	GTA Val	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
	480					485					490					
ATT Ile	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu	1718
	495				500					505					510	
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro	TTT Phe	1766
				515					520					525		
GTG Val	GAG Glu	ACG Thr	GGC Gly	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly	ACC Thr	GTC Val	1814
			530					535					540			
TCC Ser	CCC Pro	TCG Ser	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro	TAT Tyr	AGC Ser	CCT Pro	GCA Ala	GTG Val	TGG Trp	GTG Val	ATG Met	1862
			545				550					555				
ATG Met	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
	560					565					570					
GAG Glu	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys	1958
	575				580					585					590	
ACT Thr	TTC Phe	ACT Thr	ATC Ile	GGC Gly	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu	CTG Leu	TGG Trp	GCG Ala	CTG Leu	GTC Val	TTC Phe	2006
				595					600					605		
AAC Asn	AAC Asn	TCA Ser	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro	CGG Arg	GGC Gly	ACC Thr	ACC Thr	AGC Ser	AAG Lys	ATC Ile	2054
			610					615					620			
ATG Met	GTT Val	CTG Leu	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val	ATC Ile	TTC Phe	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	2102
		625					630					635				
ACG Thr	GCC Ala	AAC Asn	CTG Leu	GCC Ala	GCC Ala	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	CAA Gln	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	2150
	640					645					650					
GTG Val	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg	CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr	2198
	655				660					665					670	
CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn	GGC Gly	AGC Ser	ACG Thr	GAG Glu	CGG Arg	AAC Asn	2246
				675					680					685		
ATC Ile	CGC Arg	AGT Ser	AAC Asn	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His	ACC Thr	CAC His	ATG Met	GTC Val	AAG Lys	TTC Phe	AAC Asn	2294
			690					695					700			
CAG Gln	CGC Arg	TCG Ser	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu	ACC Thr	AGC Ser	CTC Leu	AAG Lys	ATG Met	GGC Gly	AAG Lys	GAC Asp	2342
		705				710						715				
GAG Glu	GGC Gly	TGC Cys	AAG Lys	CTG Leu	GTC Val	ACC Thr	ATT Ile	GGG Gly	TCT Ser	GGC Gly	AAG Lys	GTC Val	TTT Phe	GCT Ala	ACC Thr	2390
	720					725					730					

ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	2438
Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	
735					740					745					750	
ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	AAA	2486
Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	
				755					760						765	
CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	2534
Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	
			770					775							780	
GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	2582
Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	
			785					790								
ATG	CTG	CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	GAG	2630
Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	
	800					805					810					
CAC	CTG	GTC	TAC	TGG	AAG	CTG	CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	CAG	2678
His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	
815					820					825					830	
CTG	GAC	TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	2726
Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	
				835					840						845	
GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	CTC	2774
Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	
			850					855							860	
ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	GCC	2822
Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	
			865					870							875	
CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	2870
Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	
	880					885					890					
ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	2918
Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	
895					900					905					910	
TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	2966
Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	
				915					920						925	
CCC	GAC	CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	3014
Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	
			930					935							940	
GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	3062
Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	
			945					950							955	
CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	3110
Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	
			960				965								970	
CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	3158
Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	
				975		980				985					990	
AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	3206
Arg	His	Leu	Ser		Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	
				995						1000					1005	

TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro 1010 1015 1020	3254	
CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro 1025 1030 1035	3302	
GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CCG Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg 1040 1045 1050	3350	
GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala 1055 1060 1065 1070	3398	
TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys 1075 1080 1085	3446	
GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln 1090 1095 1100	3494	
TCG ATG TGC TTG CCG ATC TAC CCG GAG GCC TGC CAG GAG GGC GAG CAG Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln 1105 1110 1115	3542	
GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala 1120 1125 1130	3590	
CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro 1135 1140 1145 1150	3638	
CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu 1155 1160 1165	3686	
GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser 1170 1175 1180	3734	
GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe 1185 1190 1195	3782	
CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1200 1205 1210	3830	
<td>TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT</td> <td>3890</td>	TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT	3890
<td>TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC</td> <td>3950</td>	TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC	3950
<td>CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA</td> <td>4002</td>	CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4002

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1214 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gly	Gly	Ala	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Leu	Phe	Gly	1	5	10	15
Ala	Trp	Ala	Gly	Leu	Gly	Pro	Gly	Gln	Gly	Glu	Gln	Gly	Met	Thr	Val	20	25	30	
Ala	Val	Val	Phe	Ser	Ser	Ser	Gly	Pro	Pro	Gln	Ala	Gln	Phe	Arg	Val	35	40	45	
Arg	Leu	Thr	Pro	Gln	Ser	Phe	Leu	Asp	Leu	Pro	Leu	Glu	Ile	Gln	Pro	50	55	60	
Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	Ser	Leu	Leu	Thr	Gln	65	70	75	80
Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	Gly	Ile	Val	Phe	Glu	85	90	95	
Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser	100	105	110	
Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	Ala	Val	115	120	125	
Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	Gly	Val	130	135	140	
Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	Glu	Tyr	145	150	155	160
Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	His	Ala	165	170	175	
Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	Val	Ser	180	185	190	
Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	Gly	Pro	195	200	205	
Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	Val	Phe	210	215	220	
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala	225	230	235	240
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn	245	250	255	
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	260	265	270	
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	275	280	285	
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	290	295	300	
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His	305	310	315	320
Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu	325	330	335	
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr	340	345	350	

Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu	355	360	365
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr	370	375	380
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser	385	390	395
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	405	410	415
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro	420	425	430
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro	435	440	445
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	450	455	460
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	465	470	475
Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	485	490	495
Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	500	505	510
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	515	520	525
Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	530	535	540
Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	545	550	555
Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr	565	570	575
Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Thr	Phe	580	585	590
Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn	595	600	605
Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	610	615	620
Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala	625	630	635
Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser	645	650	655
Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro	660	665	670
Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	675	680	685
Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg	690	695	700

Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Asp	Glu	Gly	705	710	715	720
Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	725	730	735	
Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	740	745	750	
Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	755	760	765	
Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	770	775	780	
Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	785	790	795	800
Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	805	810	815	
Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	820	825	830	
Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	835	840	845	
Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	850	855	860	
Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	865	870	875	880
Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	885	890	895	
Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	900	905	910	
Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	915	920	925	
Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	930	935	940	
Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	945	950	955	960
Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	965	970	975	
Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	980	985	990	
Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	995	1000	1005	
Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	Arg	Pro	Phe	Leu	Pro	Leu	Phe	1010	1015	1020	
Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	Pro	Leu	Leu	Gly	Pro	Glu	Gln	1025	1030	1035	1040
Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	Ala	Ala	Trp	Ala	Arg	Gly	Ser	1045	1050	1055	

Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala  
 1060 1065 1070

Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg  
 1075 1080 1085

Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met  
 1090 1095 1100

Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly  
 1105 1110 1115 1120

Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala  
 1125 1130 1135

His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys  
 1140 1145 1150

Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His  
 1155 1160 1165

Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly  
 1170 1175 1180

Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly  
 1185 1190 1195 1200

Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val  
 1205 1210

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210...4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAACAAAA TTTACGCTAA ATTGGATTTT	60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA	120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC	180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT	233
Met Lys Pro Arg Ala Glu Cys Cys	
1 5	
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC	281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser	
10 15 20	
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC	329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile	
25 30 35 40	

CTC	GTG	GGC	ACT	TCC	GAC	GAG	GTG	GCC	ATC	AAG	GAT	GCC	CAC	GAG	AAA	377
Leu	Val	Gly	Thr	Ser	Asp	Glu	Val	Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	
				45					50					55		
GAT	GAT	TTC	CAC	CAT	CTC	TCC	GTG	GTA	CCC	CGG	GTG	GAA	CTG	GTA	GCC	425
Asp	Asp	Phe	His	His	Leu	Ser	Val	Val	Pro	Arg	Val	Glu	Leu	Val	Ala	
		60						65					70			
ATG	AAT	GAG	ACC	GAC	CCA	AAG	AGC	ATC	ATC	ACC	CGC	ATC	TGT	GAT	CTC	473
Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser	Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	
		75					80					85				
ATG	TCT	GAC	CGG	AAG	ATC	CAG	GGG	GTG	GTG	TTT	GCT	GAT	GAC	ACA	GAC	521
Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly	Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	
	90					95					100					
CAG	GAA	GCC	ATC	GCC	CAG	ATC	CTC	GAT	TTC	ATT	TCA	GCA	CAG	ACT	CTC	569
Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	
105					110					115					120	
ACC	CCG	ATC	CTG	GGC	ATC	CAC	GGG	GGC	TCC	TCT	ATG	ATA	ATG	GCA	GAT	617
Thr	Pro	Ile	Leu	Gly	Ile	His	Gly	Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	
				125					130					135		
AAG	GAT	GAA	TCC	TCC	ATG	TTC	TTC	CAG	TTT	GGC	CCA	TCA	ATT	GAA	CAG	665
Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe	Gln	Phe	Gly	Pro	Ser	Ile	Glu	Gln	
			140					145					150			
CAA	GCT	TCC	GTA	ATG	CTC	AAC	ATC	ATG	GAA	GAA	TAT	GAC	TGG	TAC	ATC	713
Gln	Ala	Ser	Val	Met	Leu	Asn	Ile	Met	Glu	Glu	Tyr	Asp	Trp	Tyr	Ile	
		155					160					165				
TTT	TCT	ATC	GTG	ACC	ACC	TAT	TTC	CCT	GGC	TAC	CAG	GAC	TTT	GTA	AAC	761
Phe	Ser	Ile	Val	Thr	Thr	Tyr	Phe	Pro	Gly	Tyr	Gln	Asp	Phe	Val	Asn	
	170					175					180					
AAG	ATC	CGC	AGC	ACC	ATT	GAG	AAT	AGC	TTT	GTG	GGC	TGG	GAG	CTA	GAG	809
Lys	Ile	Arg	Ser	Thr	Ile	Glu	Asn	Ser	Phe	Val	Gly	Trp	Glu	Leu	Glu	
	185				190					195					200	
GAG	GTG	CTC	CTA	CTG	GAC	ATG	TCC	CTG	GAC	GAT	GGA	GAT	TCT	AAG	ATC	857
Glu	Val	Leu	Leu	Leu	Asp	Met	Ser	Leu	Asp	Asp	Gly	Asp	Ser	Lys	Ile	
				205					210					215		
CAG	AAT	CAG	CTC	AAG	AAA	CTT	CAA	AGC	CCC	ATC	ATT	CTT	CTT	TAC	TGT	905
Gln	Asn	Gln	Leu	Lys	Lys	Leu	Gln	Ser	Pro	Ile	Ile	Leu	Leu	Tyr	Cys	
			220					225					230			
ACC	AAG	GAA	GAA	GCC	ACC	TAC	ATC	TTT	GAA	GTG	GCC	AAC	TCA	GTA	GGG	953
Thr	Lys	Glu	Glu	Ala	Thr	Tyr	Ile	Phe	Glu	Val	Ala	Asn	Ser	Val	Gly	
			235				240					245				
CTG	ACT	GGC	TAT	GGC	TAC	ACG	TGG	ATC	GTG	CCC	AGT	CTG	GTG	GCA	GGG	1001
Leu	Thr	Gly	Tyr	Gly	Tyr	Thr	Trp	Ile	Val	Pro	Ser	Leu	Val	Ala	Gly	
	250					255					260					
GAT	ACA	GAC	ACA	GTG	CCT	GCG	GAG	TTC	CCC	ACT	GGG	CTC	ATC	TCT	GTA	1049
Asp	Thr	Asp	Thr	Val	Pro	Ala	Glu	Phe	Pro	Thr	Gly	Leu	Ile	Ser	Val	
	265				270					275					280	
TCA	TAT	GAT	GAA	TGG	GAC	TAT	GGC	CTC	CCC	CCC	AGA	GTG	AGA	GAT	GGA	1097
Ser	Tyr	Asp	Glu	Trp	Asp	Tyr	Gly	Leu	Pro	Pro	Arg	Val	Arg	Asp	Gly	
			285						290					295		
ATT	GCC	ATA	ATC	ACC	ACT	GCT	GCT	TCT	GAC	ATG	CTG	TCT	GAG	CAC	AGC	1145
Ile	Ala	Ile	Ile	Thr	Thr	Ala	Ala	Ser	Asp	Met	Leu	Ser	Glu	His	Ser	
			300					305					310			



TTC	ATC	CCT	GAG	CCC	AAA	AGC	AGT	TGT	TAC	AAC	ACC	CAC	GAG	AAG	AGA	1193
Phe	Ile	Pro	Glu	Pro	Lys	Ser	Ser	Cys	Tyr	Asn	Thr	His	Glu	Lys	Arg	
		315					320					325				
ATC	TAC	CAG	TCC	AAT	ATG	CTA	AAT	AGG	TAT	CTG	ATC	AAT	GTC	ACT	TTT	1241
Ile	Tyr	Gln	Ser	Asn	Met	Leu	Asn	Arg	Tyr	Leu	Ile	Asn	Val	Thr	Phe	
	330					335					340					
GAG	GGG	AGG	AAT	TTG	TCC	TTC	AGT	GAA	GAT	GGC	TAC	CAG	ATG	CAC	CCG	1289
Glu	Gly	Arg	Asn	Leu	Ser	Phe	Ser	Glu	Asp	Gly	Tyr	Gln	Met	His	Pro	
345					350					355					360	
AAA	CTG	GTG	ATA	ATT	CTT	CTG	AAC	AAG	GAG	AGG	AAG	TGG	GAA	AGG	GTG	1337
Lys	Leu	Val	Ile	Ile	Leu	Leu	Asn	Lys	Glu	Arg	Lys	Trp	Glu	Arg	Val	
			365						370					375		
GGG	AAG	TGG	AAA	GAC	AAG	TCC	CTG	CAG	ATG	AAG	TAC	TAT	GTG	TGG	CCC	1385
Gly	Lys	Trp	Lys	Asp	Lys	Ser	Leu	Gln	Met	Lys	Tyr	Tyr	Val	Trp	Pro	
			380					385					390			
CGA	ATG	TGT	CCA	GAG	ACT	GAA	GAG	CAG	GAG	GAT	GAC	CAT	CTG	AGC	ATT	1433
Arg	Met	Cys	Pro	Glu	Thr	Glu	Glu	Gln	Glu	Asp	Asp	His	Leu	Ser	Ile	
		395					400					405				
GTG	ACC	CTG	GAG	GAG	GCA	CCA	TTT	GTC	ATT	GTG	GAA	AGT	GTG	GAC	CCT	1481
Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe	Val	Ile	Val	Glu	Ser	Val	Asp	Pro	
	410					415					420					
CTG	AGT	GGA	ACC	TGC	ATG	AGG	AAC	ACA	GTC	CCC	TGC	CAA	AAA	CGC	ATA	1529
Leu	Ser	Gly	Thr	Cys	Met	Arg	Asn	Thr	Val	Pro	Cys	Gln	Lys	Arg	Ile	
425					430					435					440	
GTC	ACT	GAG	AAT	AAA	ACA	GAC	GAG	GAG	CCG	GGT	TAC	ATC	AAA	AAA	TGC	1577
Val	Thr	Glu	Asn	Lys	Thr	Asp	Glu	Glu	Pro	Gly	Tyr	Ile	Lys	Lys	Cys	
				445					450					455		
TGC	AAG	GGG	TTC	TGT	ATT	GAC	ATC	CTT	AAG	AAA	ATT	TCT	AAA	TCT	GTG	1625
Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Ile	Ser	Lys	Ser	Val	
			460					465					470			
AAG	TTC	ACC	TAT	GAC	CTT	TAC	CTG	GTT	ACC	AAT	GGC	AAG	CAT	GGG	AAG	1673
Lys	Phe	Thr	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	
			475				480					485				
AAA	ATC	AAT	GGA	ACC	TGG	AAT	GGT	ATG	ATT	GGA	GAG	GTG	GTC	ATG	AAG	1721
Lys	Ile	Asn	Gly	Thr	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Met	Lys	
	490					495					500					
AGG	GCC	TAC	ATG	GCA	GTG	GGC	TCA	CTC	ACC	ATC	AAT	GAG	GAA	CGA	TCG	1769
Arg	Ala	Tyr	Met	Ala	Val	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	
505					510					515					520	
GAG	GTG	GTC	GAC	TTC	TCT	GTG	CCC	TTC	ATA	GAG	ACA	GGC	ATC	AGT	GTC	1817
Glu	Val	Val	Asp	Phe	Ser	Val	Pro	Phe	Ile	Glu	Thr	Gly	Ile	Ser	Val	
				525				530						535		
ATG	GTG	TCA	CGC	AGC	AAT	GGG	ACT	GTC	TCA	CCT	TCT	GCC	TTC	TTA	GAG	1865
Met	Val	Ser	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	
			540					545					550			
CCA	TTC	AGC	GCT	GAC	GTA	TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATC	1913
Pro	Phe	Ser	Ala	Asp	Val	Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	
			555				560					565				
GTC	TCA	GCC	GTG	GCT	GTC	TTT	GTC	TTT	GAG	TAC	TTT	AGC	CCT	GTG	GGT	1961
Val	Ser	Ala	Val	Ala	Val	Phe	Val	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Gly	
	570					575					580					

TAT Tyr 585	AAC Asn	AGG Arg	TGC Cys	CTC Leu	GCT Ala 590	GAT Asp	GGC Gly	AGA Arg	GAG Glu 595	CCT Pro	GGT Gly	GGA Gly	CCC Pro	TCT Ser	TTC Phe 600	2009
ACC Thr	ATC Ile	GGC Gly	AAA Lys	GCT Ala 605	ATT Ile	TGG Trp	TTG Leu	CTC Leu	TGG Trp 610	GGT Gly	CTG Leu	GTG Val	TTT Phe	AAC Asn 615	AAC Asn	2057
TCC Ser	GTA Val	CCT Pro	GTG Val 620	CAG Gln	AAC Asn	CCA Pro	AAG Lys	GGG Gly 625	ACC Thr	ACC Thr	TCC Ser	AAG Lys	ATC Ile 630	ATG Met	GTG Val	2105
TCA Ser	GTG Val	TGG Trp 635	GCC Ala	TTC Phe	TTT Phe	GCT Ala 640	GTC Val	ATC Ile	TTC Phe	CTG Leu	GCC Ala	AGC Ser 645	TAC Tyr	ACT Thr	GCC Ala	2153
AAC Asn 650	TTA Leu	GCT Ala	GCC Ala	TTC Phe	ATG Met 655	ATC Ile	CAA Gln 655	GAG Glu	GAA Glu	TAT Tyr 660	GTG Val 660	GAC Asp	CAG Gln	GTT Val	TCT Ser	2201
GGC Gly 665	CTG Leu	AGC Ser	GAC Asp	AAA Lys 670	AAG Lys	TTC Phe	CAG Gln	AGA Arg	CCT Pro 675	AAT Asn 675	GAC Asp	TTC Phe	TCA Ser	CCC Pro	CCT Pro 680	2249
TTC Phe	CGC Arg	TTT Phe	GGG Gly	ACC Thr 685	GTG Val	CCC Pro	AAC Asn	GGC Gly 690	AGC Ser 690	ACA Thr	GAG Glu	AGA Arg	AAT Asn 695	ATT Ile 695	CGC Arg	2297
AAT Asn	AAC Asn	TAT Tyr 700	GCA Ala 700	GAA Glu	ATG Met	CAT His	GCC Ala 705	TAC Tyr 705	ATG Met	GGA Gly	AAG Lys	TTC Phe 710	AAC Asn 710	CAG Gln	AGG Arg	2345
GGT Gly 715	GTA Val	GAT Asp 715	GAT Asp	GCA Ala	TTG Leu	CTC Leu	TCC Ser 720	CTG Leu	AAA Lys	ACA Thr	GGG Gly 725	AAA Lys 725	CTG Leu	GAT Asp	GCC Ala	2393
TTC Phe 730	ATC Ile 730	TAT Tyr	GAT Asp	GCA Ala	GCA Ala	GTG Val 735	CTG Leu	AAC Asn	TAT Tyr	ATG Met	GCA Ala 740	GGC Gly	AGA Arg	GAT Asp	GAA Glu	2441
GGC Gly 745	TGC Cys	AAG Lys	CTG Leu	GTG Val	ACC Thr 750	ATT Ile	GGC Gly	AGT Ser	GGG Gly 755	AAG Lys 755	GTC Val	TTT Phe	GCT Ala	TCC Ser	ACT Thr 760	2489
GGC Gly 765	TAT Tyr	GGC Gly	ATT Ile	GCC Ala 765	ATC Ile	CAA Gln	AAA Lys	GAT Asp 770	TCT Ser 770	GGG Gly	TGG Trp	AAG Lys	CGC Arg	CAG Gln 775	GTG Val	2537
GAC Asp	CTT Leu	GCT Ala	ATC Ile	CTG Leu	CAG Gln	CTC Leu	TTT Phe	GGA Gly 785	GAT Asp 785	GGG Gly	GAG Glu	ATG Met	GAA Glu 790	GAA Glu	CTG Leu	2585
GAA Glu	GCT Ala	CTC Leu	TGG Trp	CTC Leu	ACT Thr	GGC Gly 800	ATT Ile	TGT Cys	CAC His	AAT Asn	GAG Glu	AAG Lys 805	AAT Asn	GAG Glu	GTC Val	2633
ATG Met 810	AGC Ser	AGC Ser	CAG Gln	CTG Leu	GAC Asp 815	ATT Ile	GAC Asp	AAC Asn	ATG Met	GCA Ala	GGG Gly 820	GTC Val	TTC Phe	TAC Tyr	ATG Met	2681
TTG Leu 825	GGG Gly	GCG Ala	GCC Ala	ATG Met 830	GCT Ala	CTC Leu	AGC Ser	CTC Leu	ATC Ile	ACC Thr 835	TTC Phe	ATC Ile	TGC Cys	GAA Glu	CAC His 840	2729
CTT Leu	TTC Phe	TAT Tyr	TGG Trp	CAG Gln 845	TTC Phe	CGA Arg	CAT His	TGC Cys 850	TTT Phe 850	ATG Met	GGT Gly	GTC Val	TGT Cys	TCT Ser	GGC Gly 855	2777

AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC	2825
Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile	
860 865 870	
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC	2873
His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr	
875 880 885	
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG	2921
Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr	
890 895 900	
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC	2969
Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser	
905 910 915 920	
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG	3017
Ala Leu Asp Phe Ile Arg Arg Glu Ser Val Tyr Asp Ile Ser Glu	
925 930 935	
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG	3065
His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro	
940 945 950	
CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA	3113
Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg	
955 960 965	
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC	3161
Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His	
970 975 980	
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC	3209
Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile	
985 990 995 1000	
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG	3257
Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg	
1005 1010 1015	
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC	3305
Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His	
1020 1025 1030	
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC	3353
Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg	
1035 1040 1045	
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA	3401
Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser	
1050 1055 1060	
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG	3449
Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg	
1065 1070 1075 1080	
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC	3497
Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala	
1085 1090 1095	
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA	3545
Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg	
1100 1105 1110	
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG	3593
Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly	
1115 1120 1125	

CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881
TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAG ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409

AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val 148	4701
TAAGGCTGTG GGTGCGGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTC	4761
CATTTGCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
GGGCAACCTCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC	4881
CCGCTGTGAG CCATTCTCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAAGGAGG	4941
GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGSTGTGGAA GAGCTCCTTG	5001
ATATCTCTTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
TTTTCCCAA CTGATCTTTT CATTTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT	5121
TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT	5181
CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTSTTTA TATATAAGCC	5241
CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC	5301
ATTGGTGGCA GAGTGGATTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG	5361
TGCCTTG3GG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGCACC	5421
CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT	5481
CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC	5538

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Lys	Pro	Arg	Ala	Glu	Cys	Cys	Ser	Pro	Lys	Phe	Trp	Leu	Val	Leu
1				5					10					15	

Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro  
20 25 30

Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val  
35 40 45

Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val  
50 55 60

Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser  
65 70 75 80

Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly  
85 90 95

Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu  
100 105 110

Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly  
115 120 125

Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe  
130 135 140

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile  
145 150 155 160

Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe  
165 170 175

Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn  
180 185 190

Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser  
195 200 205

Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln  
210 215 220

Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile  
225 230 235 240

Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp  
245 250 255

Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu  
260 265 270

Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly  
275 280 285

Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala  
290 295 300

Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser  
305 310 315 320

Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn  
325 330 335

Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser  
340 345 350

Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn  
355 360 365

Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu

370	375	380
Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu 385 390 395 400		
Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe 405 410 415		
Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn 420 425 430		
Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu 435 440 445		
Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile 450 455 460		
Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu 465 470 475 480		
Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly 485 490 495		
Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser 500 505 510		
Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro 515 520 525		
Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr 530 535 540		
Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val 545 550 555 560		
Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val 565 570 575		
Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly 580 585 590		
Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu 595 600 605		
Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys 610 615 620		
Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val 625 630 635 640		
Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln 645 650 655		
Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln 660 665 670		
Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn 675 680 685		
Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala 690 695 700		
Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser 705 710 715 720		
Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu 725 730 735		

Asn	Tyr	Met	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	
			740					745					750			
Ser	Gly	Lys	Val	Phe	Ala	Ser	Thr	Gly	Tyr	Gly	Ile	Ala	Ile	Gln	Lys	
		755					760					765				
Asp	Ser	Gly	Trp	Lys	Arg	Gln	Val	Asp	Leu	Ala	Ile	Leu	Gln	Leu	Phe	
	770					775					780					
Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Ala	Leu	Trp	Leu	Thr	Gly	Ile	
785					790					795					800	
Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	Ile	Asp	
			805						810					815		
Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Gly	Ala	Ala	Met	Ala	Leu	Ser	
		820						825					830			
Leu	Ile	Thr	Phe	Ile	Cys	Glu	His	Leu	Phe	Tyr	Trp	Gln	Phe	Arg	His	
		835					840					845				
Cys	Phe	Met	Gly	Val	Cys	Ser	Gly	Lys	Pro	Gly	Met	Val	Phe	Ser	Ile	
	850					855					860					
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	Ala	Ile	Glu	Glu	Arg	
865					870					875					880	
Gln	Ser	Val	Met	Asn	Ser	Pro	Thr	Ala	Thr	Met	Asn	Asn	Thr	His	Ser	
				885					890					895		
Asn	Ile	Leu	Arg	Leu	Leu	Arg	Thr	Ala	Lys	Asn	Met	Ala	Asn	Leu	Ser	
		900						905					910			
Gly	Val	Asn	Gly	Ser	Pro	Gln	Ser	Ala	Leu	Asp	Phe	Ile	Arg	Arg	Glu	
		915					920					925				
Ser	Ser	Val	Tyr	Asp	Ile	Ser	Glu	His	Arg	Arg	Ser	Phe	Thr	His	Ser	
	930					935					940					
Asp	Cys	Lys	Ser	Tyr	Asn	Asn	Pro	Pro	Cys	Glu	Glu	Asn	Leu	Phe	Ser	
945					950					955					960	
Asp	Tyr	Ile	Ser	Glu	Val	Glu	Arg	Thr	Phe	Gly	Asn	Leu	Gln	Leu	Lys	
				965					970					975		
Asp	Ser	Asn	Val	Tyr	Gln	Asp	His	Tyr	His	His	His	His	Arg	Pro	His	
		980						985					990			
Ser	Ile	Gly	Ser	Ala	Ser	Ser	Ile	Asp	Gly	Leu	Tyr	Asp	Cys	Asp	Asn	
		995					1000					1005				
Pro	Pro	Phe	Thr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Lys	Lys	Pro	Leu	Asp	
	1010					1015					1020					
Ile	Gly	Leu	Pro	Ser	Ser	Lys	His	Ser	Gln	Leu	Ser	Asp	Leu	Tyr	Gly	
1025					1030					1035					1040	
Lys	Phe	Ser	Phe	Lys	Ser	Asp	Arg	Tyr	Ser	Gly	His	Asp	Asp	Leu	Ile	
				1045					1050					1055		
Arg	Ser	Asp	Val	Ser	Asp	Ile	Ser	Thr	His	Thr	Val	Thr	Tyr	Gly	Asn	
			1060					1065					1070			
Ile	Glu	Gly	Asn	Ala	Ala	Lys	Arg	Arg	Lys	Gln	Gln	Tyr	Lys	Asp	Ser	
		1075					1080					1085				
Leu	Lys	Lys	Arg	Pro	Ala	Ser	Ala	Lys	Ser	Arg	Arg	Glu	Phe	Asp	Glu	



1090	1095	1100
Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys 1105 1110 1115 1120		
Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln 1125 1130 1135		
Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr 1140 1145 1150		
Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser 1155 1160 1165		
Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly 1170 1175 1180		
Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn 1185 1190 1195 1200		
Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg 1205 1210 1215		
Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln 1220 1225 1230		
Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala 1235 1240 1245		
Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp 1250 1255 1260		
Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys 1265 1270 1275 1280		
Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn 1285 1290 1295		
Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys 1300 1305 1310		
Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly 1315 1320 1325		
Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala 1330 1335 1340		
Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly 1345 1350 1355 1360		
His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser 1365 1370 1375		
Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly 1380 1385 1390		
Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln 1395 1400 1405		
Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu 1410 1415 1420		
Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala 1425 1430 1435 1440		
Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val 1445 1450 1455		

Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His  
 1460 1465 1470  
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val  
 1475 1480

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4695 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCCA	180
GAAACATGTG TGGCCACCTC CTCGCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
GGCTCTCTGA GCCCTCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTC GGTCCTGGCC	420
CCCCCGCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	
20 25 30	
GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG	625
Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
35 40 45	
GCG CCG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser	
65 70 75	
CCG GGC CTA GAC GTG CCG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGC TTG CGC	817
Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	

100								105								110	
GTG	CAC	GGC	GTG	GTC	TTC	GAA	GAC	GAC	TCG	CGC	GCG	CCC	GCC	GTC	GCG	865	
Val	His	Gly	Val	Val	Phe	Glu	Asp	Asp	Ser	Arg	Ala	Pro	Ala	Val	Ala		
115								120								125	
CCC	ATC	CTC	GAC	TTC	CTG	TCG	GCG	CAG	ACC	TCG	CTC	CCC	ATC	GTG	TCC	913	
Pro	Ile	Leu	Asp	Phe	Leu	Ser	Ala	Gln	Thr	Ser	Leu	Pro	Ile	Val	Ser		
130								135								140	
GAG	CAC	GGC	GGC	GCC	GCG	CTC	GTG	CTC	ACG	CCC	AAG	GAG	AAG	GGC	TCC	961	
Glu	His	Gly	Gly	Ala	Ala	Leu	Val	Leu	Thr	Pro	Lys	Glu	Lys	Gly	Ser		
145								150								155	
ACC	TTC	CTC	CAC	CTG	GGC	TCT	TCC	CCC	GAG	CAA	CAG	CTT	CAG	GTC	ATC	1009	
Thr	Phe	Leu	His	Leu	Gly	Ser	Ser	Pro	Glu	Gln	Gln	Leu	Gln	Val	Ile		
160								165								170	
TTT	GAG	GTG	CTG	GAG	GAG	TAT	GAC	TGG	ACG	TCC	TTT	GTA	GCC	GTG	ACC	1057	
Phe	Glu	Val	Leu	Glu	Glu	Tyr	Asp	Trp	Thr	Ser	Phe	Val	Ala	Val	Thr		
180								185								190	
ACT	CGT	GCC	CCT	GGC	CAC	CGG	GCC	TTC	CTG	TCC	TAC	ATT	GAG	GTG	CTG	1105	
Thr	Arg	Ala	Pro	Gly	His	Arg	Ala	Phe	Leu	Ser	Tyr	Ile	Glu	Val	Leu		
195								200								205	
ACT	GAC	GGC	AGT	CTG	GTG	GGC	TGG	GAG	CAC	CGC	GGA	GCG	CTG	ACG	CTG	1153	
Thr	Asp	Gly	Ser	Leu	Val	Gly	Trp	Glu	His	Arg	Gly	Ala	Leu	Thr	Leu		
210								215								220	
GAC	CCT	GGG	GCG	GGC	GAG	GCC	GTG	CTC	AGT	GCC	CAG	CTC	CGC	AGT	GTC	1201	
Asp	Pro	Gly	Ala	Gly	Glu	Ala	Val	Leu	Ser	Ala	Gln	Leu	Arg	Ser	Val		
225								230								235	
AGC	GCG	CAG	ATC	CGC	CTG	CTC	TTC	TGC	GCC	CGA	GAG	GAG	GCC	GAG	CCC	1249	
Ser	Ala	Gln	Ile	Arg	Leu	Leu	Phe	Cys	Ala	Arg	Glu	Glu	Ala	Glu	Pro		
240								245								250	
GTG	TTC	CGC	GCA	GCT	GAG	GAG	GCT	GGC	CTC	ACT	GGA	TCT	GGC	TAC	GTC	1297	
Val	Phe	Arg	Ala	Ala	Glu	Glu	Ala	Gly	Leu	Thr	Gly	Ser	Gly	Tyr	Val		
260								265								270	
TGG	TTC	ATG	GTG	GGG	CCC	CAG	CTG	GCT	GGA	GGC	GGG	GGC	TCT	GGG	GCC	1345	
Trp	Phe	Met	Val	Gly	Pro	Gln	Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ala		
275								280								285	
CCT	GGT	GAG	CCC	CCT	CTT	CTG	CCA	GGA	GGC	GCC	CCC	CTG	CCT	GCC	GGG	1393	
Pro	Gly	Glu	Pro	Pro	Leu	Leu	Pro	Gly	Gly	Ala	Pro	Leu	Pro	Ala	Gly		
290								295								300	
CTG	TTT	GCA	GTG	CGC	TCG	GCT	GGC	TGG	CGG	GAT	GAC	CTG	GCT	CGG	CGA	1441	
Leu	Phe	Ala	Val	Arg	Ser	Ala	Gly	Trp	Arg	Asp	Asp	Leu	Ala	Arg	Arg		
305								310								315	
GTG	GCA	GCT	GGC	GTG	GCC	GTA	GTG	GCC	AGA	GGT	GCC	CAG	GCC	CTG	CTG	1489	
Val	Ala	Ala	Gly	Val	Ala	Val	Val	Ala	Arg	Gly	Ala	Gln	Ala	Leu	Leu		
320								325								330	
CGT	GAT	TAT	GGT	TTC	CTT	CCT	GAG	CTC	GGC	CAC	GAC	TGT	CGC	GCC	CAG	1537	
Arg	Asp	Tyr	Gly	Phe	Leu	Pro	Glu	Leu	Gly	His	Asp	Cys	Arg	Ala	Gln		
340								345								350	
AAC	CGC	ACC	CAC	CGC	GGG	GAG	AGT	CTG	CAT	AGG	TAC	TTC	ATG	AAC	ATC	1585	
Asn	Arg	Thr	His	Arg	Gly	Glu	Ser	Leu	His	Arg	Tyr	Phe	Met	Asn	Ile		
355								360								365	
ACG	TGG	GAT	AAC	CGG	GAT	TAC	TCC	TTC	AAT	GAG	GAC	GGC	TTC	CTA	GTG	1633	

Thr	Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	
		370					375					380				
AAC	CCC	TCC	CTG	GTG	GTC	ATC	TCC	CTC	ACC	AGA	GAC	AGG	ACG	TGG	GAG	1681
Asn	Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	
	385					390					395					
GTG	GTG	GGC	AGC	TGG	GAG	CAG	CAG	ACG	CTC	CGC	CTC	AAG	TAC	CCG	CTG	1729
Val	Val	Gly	Ser	Trp	Glu	Gln	Gln	Thr	Leu	Arg	Leu	Lys	Tyr	Pro	Leu	
400					405					410					415	
TGG	TCC	CGC	TAT	GGT	CGC	TTC	CTG	CAG	CCA	GTG	GAC	GAC	ACG	CAG	CAC	1777
Trp	Ser	Arg	Tyr	Gly	Arg	Phe	Leu	Gln	Pro	Val	Asp	Asp	Thr	Gln	His	
				420					425					430		
CTC	GCG	GTG	GCC	ACG	CTG	GAG	GAA	AGG	CCG	TTT	GTC	ATC	GTG	GAG	CCT	1825
Leu	Ala	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Pro	
			435					440					445			
GCA	GAC	CCT	ATC	AGC	GGC	ACC	TGC	ATC	CGA	GAC	TCC	GTC	CCC	TGC	CGG	1873
Ala	Asp	Pro	Ile	Ser	Gly	Thr	Cys	Ile	Arg	Asp	Ser	Val	Pro	Cys	Arg	
		450					455					460				
AGC	CAG	CTC	AAC	CGA	ACC	CAC	AGC	CCT	CCA	CCG	GAT	GCC	CCC	CGC	CCG	1921
Ser	Gln	Leu	Asn	Arg	Thr	His	Ser	Pro	Pro	Pro	Asp	Ala	Pro	Arg	Pro	
	465					470					475					
GAA	AAG	CGC	TGC	TGC	AAG	GGT	TTC	TGC	ATC	GAC	ATT	CTG	AAG	CGG	CTG	1969
Glu	Lys	Arg	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Arg	Leu	
480					485					490					495	
GCG	CAT	ACC	ATC	GGC	TTC	AGC	TAC	GAC	CTC	TAC	CTG	GTC	ACC	AAT	GGC	2017
Ala	His	Thr	Ile	Gly	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	
				500					505					510		
AAG	CAC	GGA	AAG	AAG	ATC	GAT	GGC	GTC	TGG	AAC	GGC	ATG	ATC	GGG	GAG	2065
Lys	His	Gly	Lys	Lys	Ile	Asp	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	
			515					520					525			
GTG	TTC	TAC	CAG	CGC	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAC	2113
Val	Phe	Tyr	Gln	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	
		530					535					540				
GAG	GAG	CGC	TCC	GAG	ATC	GTG	GAC	TTC	TCC	GTC	CCC	TTC	GTG	GAG	ACC	2161
Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	
		545				550					555					
GGC	ATC	AGC	GTC	ATG	GTG	GCG	CGC	AGC	AAT	GGC	ACG	GTG	TCC	CCC	TCG	2209
Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	
				565						570					575	
GCC	TTC	CTC	GAG	CCC	TAC	AGC	CCC	GCC	GTG	TGG	GTG	ATG	ATG	TTC	GTC	2257
Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	
				580					585					590		
ATG	TGC	CTC	ACT	GTG	GTC	GCC	GTC	ACT	GTT	TTC	ATC	TTC	GAG	TAC	CTC	2305
Met	Cys	Leu	Thr	Val	Val	Ala	Val	Thr	Val	Phe	Ile	Phe	Glu	Tyr	Leu	
				595				600					605			
AGT	CCT	GTT	GGT	TAC	AAC	CGC	AGC	CTG	GCC	ACG	GGC	AAG	CGC	CCT	GGC	2353
Ser	Pro	Val	Gly	Tyr	Asn	Arg	Ser	Leu	Ala	Thr	Gly	Lys	Arg	Pro	Gly	
		610					615					620				
GGT	TCA	ACC	TTC	ACC	ATT	GGG	AAA	TCC	ATC	TGG	CTG	CTC	TGG	GCC	CTG	2401
Gly	Ser	Thr	Phe	Thr	Ile	Gly	Lys	Ser	Ile	Trp	Leu	Leu	Trp	Ala	Leu	
		625				630					635					

GTG	TTC	AAT	AAT	TGG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC	2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	
640					645					650					655	
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC	2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	
				660					665					670		
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG	2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	
			675					680					685			
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG	2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu	
		690					695					700				
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG	2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	
	705					710					715					
AAG	AAC	ATC	CGC	AGC	AAC	TAT	CCC	GAC	ATG	CAC	AGC	TAC	ATG	GTG	CGC	2689
Lys	Asn	Ile	Arg	Ser	Asn	Tyr	Pro	Asp	Met	His	Ser	Tyr	Met	Val	Arg	
720					725				730						735	
TAC	AAC	CAG	CCC	CGC	GTA	GAG	GAA	GCG	CTC	ACT	CAG	CTC	AAG	GCA	GGG	2737
Tyr	Asn	Gln	Pro	Arg	Val	Glu	Glu	Ala	Leu	Thr	Gln	Leu	Lys	Ala	Gly	
				740					745					750		
AAG	CTG	GAC	GCC	TTC	ATC	TAC	GAT	GCT	GCA	GTG	CTC	AAT	TAC	ATG	GCC	2785
Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	
			755					760					765			
CGC	AAG	GAC	GAG	GGC	TGC	AAG	CTT	GTC	ACC	ATC	GGC	TCC	GGC	AAG	GTC	2833
Arg	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	
		770					775					780				
TTC	GCC	ACG	ACA	GGC	TAT	GGC	ATC	GCC	CTG	CAC	AAG	GGC	TCC	CGC	TGG	2881
Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	His	Lys	Gly	Ser	Arg	Trp	
	785					790					795					
AAG	CGG	CCC	ATC	GAC	CTG	GCG	TTG	CTG	CAG	TTC	CTG	GGG	GAT	GAT	GAG	2929
Lys	Arg	Pro	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Asp	Glu	
800					805				810						815	
ATC	GAG	ATG	CTG	GAG	CGG	CTG	TGG	CTC	TCT	GGG	ATC	TGC	CAC	AAT	GAC	2977
Ile	Glu	Met	Leu	Glu	Arg	Leu	Trp	Leu	Ser	Gly	Ile	Cys	His	Asn	Asp	
				820				825						830		
AAA	ATC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GCG	GGC	3025
Lys	Ile	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Ala	Gly	
			835					840					845			
GTC	TTC	TAC	ATG	CTC	CTG	GTG	GCC	ATG	GGC	CTG	TCC	CTG	CTG	GTC	TTC	3073
Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ser	Leu	Leu	Val	Phe	
		850					855					860				
GCC	TGG	GAG	CAC	CTG	GTG	TAC	TGG	CGC	CTG	CGG	CAC	TGC	CTG	GGG	CCC	3121
Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Arg	Leu	Arg	His	Cys	Leu	Gly	Pro	
	865					870					875					
ACC	CAC	CGC	ATG	GAC	TTC	CTG	GCC	TTC	TCC	AGG	GGC	ATG	TAC	AGC		3169
Thr	His	Arg	Met	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Met	Tyr	Ser	
880					885				890					895		
TGC	TGC	AGC	GCT	GAG	GCC	GCC	CCA	CCG	CCC	GCC	AAG	CCC	CCG	CCG	CCG	3217
Cys	Cys	Ser	Ala	Glu	Ala	Ala	Pro	Pro	Pro	Ala	Lys	Pro	Pro	Pro	Pro	
				900					905					910		

CCA	CAG	CCC	CTG	CCC	AGC	CCC	GCG	TAC	CCC	GCG	CCG	GGG	CCG	GCT	CCC	3265
Pro	Gln	Pro	Leu	Pro	Ser	Pro	Ala	Tyr	Pro	Ala	Pro	Gly	Pro	Ala	Pro	
			915					920					925			
GGG	CCC	GCA	CCT	TTC	GTC	CCC	CGC	GAG	CGC	GCC	TCA	GTG	GCC	CGC	TGG	3313
Gly	Pro	Ala	Pro	Phe	Val	Pro	Arg	Glu	Arg	Ala	Ser	Val	Ala	Arg	Trp	
			930					935					940			
CGC	CGG	CCC	AAG	GGC	GCG	GGG	CCG	CCG	GGG	GCG	GCG	GCG	CTG	GCC	GAC	3361
Arg	Arg	Pro	Lys	Gly	Ala	Gly	Pro	Pro	Gly	Gly		Gly	Leu	Ala	Asp	
			945				950					955				
GGC	TTC	CAC	CGC	TAC	TAC	GGC	CCC	ATC	GAG	CCG	CAG	GGC	CTA	GGC	CTC	3409
Gly	Phe	His	Arg	Tyr	Tyr	Gly	Pro	Ile	Glu	Pro	Gln	Gly	Leu	Gly	Leu	
					965					970					975	
GGC	CTG	GGC	GAA	GCG	CGC	GCG	GCA	CCG	CGG	GCG	GCA	GCC	GGG	CGC	CCG	3457
Gly	Leu	Gly	Glu	Ala	Arg	Ala	Ala	Pro	Arg	Gly	Ala	Ala	Gly	Arg	Pro	
				980					985						990	
CTG	TCC	CCG	CCG	GCC	GCT	CAG	CCC	CCG	CAG	AAG	CCG	CCG	GCC	TCC	TAT	3505
Leu	Ser	Pro	Pro	Ala	Ala	Gln	Pro	Pro	Gln	Lys	Pro	Pro	Ala	Ser	Tyr	
				995				1000						1005		
TTC	GCC	ATC	GTA	CGC	GAC	AAG	GAG	CCA	GCC	GAG	CCC	CCC	GCC	GGC	GCC	3553
Phe	Ala	Ile	Val	Arg	Asp	Lys	Glu	Pro	Ala	Glu	Pro	Pro	Ala	Gly	Ala	
			1010					1015					1020			
TTC	CCC	GGC	TTC	CCG	TCC	CCG	CCC	GCG	CCC	CCC	GCC	GCC	GCG	GCC	ACC	3601
Phe	Pro	Gly	Phe	Pro	Ser	Pro	Pro	Ala	Pro	Pro	Ala	Ala	Ala	Ala	Thr	
			1025				1030					1035				
GCC	GTC	GGG	CCG	CCA	CTC	TGC	CGC	TTG	GCC	TTC	GAG	GAC	GAG	AGC	CCG	3649
Ala	Val	Gly	Pro	Pro	Leu	Cys	Arg	Leu	Ala	Phe	Glu	Asp	Glu	Ser	Pro	
					1045					1050					1055	
CCG	GCG	CCC	GCG	CGG	TGG	CCG	CGC	TCG	GAC	CCC	GAG	AGC	CAA	CCC	CTG	3697
Pro	Ala	Pro	Ala	Arg	Trp	Pro	Arg	Ser	Asp	Pro	Glu	Ser	Gln	Pro	Leu	
				1060					1065					1070		
CTG	GGG	CCA	GGC	GCG	GGC	GGC	GCG	GGG	GCG	ACG	GGG	GGC	GCA	GGC	GGA	3745
Leu	Gly	Pro	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	
			1075					1080					1085			
GGA	GCC	CCG	GCC	GCT	CCG	CCC	CCG	TGC	TTC	GCC	GCG	CCG	CCC	CCG	TGC	3793
Gly	Ala	Pro	Ala	Ala	Pro	Pro	Pro	Cys	Phe	Ala	Ala	Pro	Pro	Pro	Cys	
			1090					1095				1100				
TTT	TAC	CTC	GAT	GTC	GAC	CAG	TCG	CCG	TCG	GAC	TCG	GAG	GAC	TCG	GAG	3841
Phe	Tyr	Leu	Asp	Val	Asp	Gln	Ser	Pro	Ser	Asp	Ser	Glu	Asp	Ser	Glu	
			1105				1110					1115				
AGC	CTG	GCC	GGC	GCG	TCC	CTG	GCC	GGC	CTG	GAT	CCC	TGG	TGG	TTC	GCC	3889
Ser	Leu	Ala	Gly	Ala	Ser	Leu	Ala	Gly	Leu	Asp	Pro	Trp	Trp	Phe	Ala	
					1125					1130					1135	
GAC	TTC	CCT	TAC	CCG	TAT	GCC	GAT	CGC	CTC	GGG	CSG	CCC	GCG	GCA	CGC	3937
Asp	Phe	Pro	Tyr	Pro	Tyr	Ala	Asp	Arg	Leu	Gly	Xaa	Pro	Ala	Ala	Arg	
				1140					1145					1150		
TAC	GGA	TTG	GTC	GAC	AAA	CTA	GGG	GCG	TGG	CTC	GCC	GGG	AGC	TGG	GAC	3985
Tyr	Gly	Leu	Val	Asp	Lys	Leu	Gly	Gly	Trp	Leu	Ala	Gly	Ser	Trp	Asp	
			1155					1160					1165			
TAC	CTG	CCT	CCS	CGC	AGC	GGT	CGG	GCC	GCC	TGG	CAC	TGT	CGG	CAC	TGC	4033
Tyr	Leu	Pro	Xaa	Arg	Ser	Gly	Arg	Ala	Ala	Trp	His	Cys	Arg	His	Cys	
			1170				1175					1180				

GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGC CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273
CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro 1265 1270 1275	4321
CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg 1280 1285 1290 1295	4369
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser 1300 1305 1310	4417
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala 1315 1320 1325	4465
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGCCC His Phe Ser Ser Leu Glu Ser Glu Val 1330 1335	4512
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met 1 5 10 15
Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala 20 25 30
Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala

35					40					45					
Arg	Pro	Leu	Asn	Val	Ala	Leu	Val	Phe	Ser	Gly	Pro	Ala	Tyr	Ala	Ala
50					55					60					
Glu	Ala	Ala	Arg	Leu	Gly	Pro	Ala	Val	Ala	Ala	Ala	Val	Arg	Ser	Pro
65					70					75					80
Gly	Leu	Asp	Val	Arg	Pro	Val	Ala	Leu	Val	Leu	Asn	Gly	Ser	Asp	Pro
				85					90					95	
Arg	Ser	Leu	Val	Leu	Gln	Leu	Cys	Asp	Leu	Leu	Ser	Gly	Leu	Arg	Val
			100					105					110		
His	Gly	Val	Val	Phe	Glu	Asp	Asp	Ser	Arg	Ala	Pro	Ala	Val	Ala	Pro
			115				120					125			
Ile	Leu	Asp	Phe	Leu	Ser	Ala	Gln	Thr	Ser	Leu	Pro	Ile	Val	Ser	Glu
	130					135					140				
His	Gly	Gly	Ala	Ala	Leu	Val	Leu	Thr	Pro	Lys	Glu	Lys	Gly	Ser	Thr
145					150					155					160
Phe	Leu	His	Leu	Gly	Ser	Ser	Pro	Glu	Gln	Gln	Leu	Gln	Val	Ile	Phe
				165					170					175	
Glu	Val	Leu	Glu	Glu	Tyr	Asp	Trp	Thr	Ser	Phe	Val	Ala	Val	Thr	Thr
			180					185					190		
Arg	Ala	Pro	Gly	His	Arg	Ala	Phe	Leu	Ser	Tyr	Ile	Glu	Val	Leu	Thr
		195					200					205			
Asp	Gly	Ser	Leu	Val	Gly	Trp	Glu	His	Arg	Gly	Ala	Leu	Thr	Leu	Asp
	210					215					220				
Pro	Gly	Ala	Gly	Glu	Ala	Val	Leu	Ser	Ala	Gln	Leu	Arg	Ser	Val	Ser
225					230					235					240
Ala	Gln	Ile	Arg	Leu	Leu	Phe	Cys	Ala	Arg	Glu	Glu	Ala	Glu	Pro	Val
				245					250					255	
Phe	Arg	Ala	Ala	Glu	Glu	Ala	Gly	Leu	Thr	Gly	Ser	Gly	Tyr	Val	Trp
			260					265					270		
Phe	Met	Val	Gly	Pro	Gln	Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ala	Pro
		275				280						285			
Gly	Glu	Pro	Pro	Leu	Leu	Pro	Gly	Gly	Ala	Pro	Leu	Pro	Ala	Gly	Leu
	290					295					300				
Phe	Ala	Val	Arg	Ser	Ala	Gly	Trp	Arg	Asp	Asp	Leu	Ala	Arg	Arg	Val
305					310					315					320
Ala	Ala	Gly	Val	Ala	Val	Val	Ala	Arg	Gly	Ala	Gln	Ala	Leu	Leu	Arg
				325					330					335	
Asp	Tyr	Gly	Phe	Leu	Pro	Glu	Leu	Gly	His	Asp	Cys	Arg	Ala	Gln	Asn
			340					345					350		
Arg	Thr	His	Arg	Gly	Glu	Ser	Leu	His	Arg	Tyr	Phe	Met	Asn	Ile	Thr
			355				360					365			
Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	Asn
	370					375					380				
Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	Val
385					390					395					400



Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp  
415 410 415

Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu  
420 425 430

Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala  
435 440 445

Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser  
450 455 460

Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu  
465 470 475 480

Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala  
485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys  
500 505 510

His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val  
515 520 525

Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu  
530 535 540

Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly  
545 550 555 560

Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala  
565 570 575

Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met  
580 585 590

Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser  
595 600 605

Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly  
610 615 620

Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val  
625 630 635 640

Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys  
645 650 655

Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser  
660 665 670

Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp  
675 680 685

Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln  
690 695 700

Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys  
705 710 715 720

Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr  
725 730 735

Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys  
740 745 750

Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg

755		760		765
Lys Asp Glu Gly Cys Lys	Leu Val Thr Ile Gly Ser Gly Lys Val Phe			
770	775	780		
Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys				
785	790	795		800
Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile				
	805	810		815
Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys				
	820	825		830
Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val				
	835	840		845
Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala				
	850	855		860
Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr				
	865	870		875
His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys				
	885	890		895
Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro				
	900	905		910
Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly				
	915	920		925
Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg				
	930	935		940
Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly				
	945	950		955
Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly				
	965	970		975
Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu				
	980	985		990
Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe				
	995	1000		1005
Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe				
	1010	1015		1020
Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala				
	1025	1030		1035
Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro				
	1045	1050		1055
Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu				
	1060	1065		1070
Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly				
	1075	1080		1085
Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe				
	1090	1095		1100
Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser				
	1105	1110		1115
				1120

Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp  
1125 1130 1135

Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr  
1140 1145 1150

Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr  
1155 1160 1165

Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala  
1170 1175 1180

Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp  
1185 1190 1195 1200

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala Ala  
1205 1210 1215

Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His  
1220 1225 1230

Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala Pro  
1235 1240 1245

His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro  
1250 1255 1260

Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg  
1265 1270 1275 1280

Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg  
1285 1290 1295

Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His  
1300 1305 1310

Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His  
1315 1320 1325

Phe Ser Ser Leu Glu Ser Glu Val  
1330 1335

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCCT ACTCCAAGAT CTGGCCCTAG  
TCCATGTTTG C

60

71

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60  
ACTAGGGCCA G 71

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG 60  
G 61

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60  
CT 62

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCGCAGAGCA CCTCCACCAT CTCCTTGTCC TACTCCAAGA TCTGGCCCTA GTCCATGTTT 60  
GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG 120  
TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGGC 180  
TCCTTTGTCT GACGT 195